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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:42:39 ; Search time 59 Seconds

(without alignments)
 1896.421 Million cell updates/secTitle: US-10-667-442-2
 Perfect score: 2104
 Sequence: 1 MGANTSRKPPVFDENEDVNFI.....NLALEQTKDPOQGDGGNNNL 396Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summariesDatabase : A_Geneseq_29Jan04:
 1: GeneseqP1980s:
 2: GeneseqP1990s:
 3: GeneseqP2000s:
 4: GeneseqP2001s:
 5: GeneseqP2002s:
 6: GeneseqP2003as:
 7: GeneseqP2003bs:
 8: GeneseqP2004s:
 8:

ALIGNMENTS

RESULT 1
 ABG70700
 ID ABG70700 standard; protein; 396 AA.

XX ABG70700;
 XX DT 17-JAN-2003 (first entry)
 XX DB Human serine/threonine protein kinase-like kinase.
 XX KW Human; kinase; serine/threonine kinase; immune response; transgenic;
 KW enzyme.
 XX OS Homo sapiens.
 XX Key
 PT Modified-site 2. .7
 FT Modified-site /label= N_myristoylation_site
 FT Modified-site 4. .7
 FT Modified-site /label= N_glycosylation_site
 FT Modified-site 5. .7
 FT Modified-site /label= Protein_kinase_C_phosphorylation_site
 FT Modified-site 6. .8
 FT Modified-site /label= Protein_kinase_ATP-binding_region
 FT Modified-site 29. .52
 FT Binding-site /label= Protein_kinase_C_phosphorylation_site
 FT Modified-site 33. .36
 FT Modified-site /label= Casein_kinase_II_phosphorylation_site
 FT Modified-site 43. .46
 FT Modified-site /label= N_glycosylation_site
 FT Modified-site 45. .47
 FT Modified-site /label= Protein_kinase_C_phosphorylation_site
 FT Modified-site 89. .92
 FT Modified-site /label= Casein_kinase_II_phosphorylation_site
 FT Modified-site 122. .124
 FT Modified-site /label= Protein_kinase_C_phosphorylation_site
 FT Modified-site 142. .154
 FT Active-site /label= Serine/threonine_protein_kinase_active_site
 FT Modified-site 197. .202
 FT Modified-site /label= N_myristoylation_site
 FT Modified-site 194. .196
 FT Modified-site /label= Protein_kinase_C_phosphorylation_site
 FT Modified-site 212. .215
 FT Modified-site /label= Casein_kinase_II_phosphorylation_site
 FT Modified-site 218. .221
 FT Modified-site /label= Amidation_site

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2104	100.0	396	6	ABG70700		Abg70700 Human ser
2	2104	100.0	396	6	ABU62276		Abu62276 Human kin
3	2089	99.3	396	4	AAB85491		Aab85491 Human pro
4	2089	99.3	396	5	JAE14261		Aae14261 Novel hum
5	2089	99.3	396	5	AAB21725		Aae21725 Human PKI
6	2083	99.0	396	5	AAM50334		Aam50334 Human 149
7	2047	97.3	407	5	JAE14260		Aae14260 Novel hum
8	1500.5	71.3	327	4	AAU03504		Aau03504 Human pro
9	1427	67.8	404	6	ABU62277		Abu62277 Mouse ser
10	1425.5	67.8	403	6	ABU62278		Abu62278 Human ser
11	1425.5	67.8	414	4	AAB65600		Aab65600 Novel pro
12	1425.5	67.8	414	5	ABP43807		Abp43807 Serine/th
13	1425.5	67.8	414	5	AAO17710		Aao17710 Human ser
14	1425.5	67.8	414	6	AAB58617		Abr58617 Human can
15	1425.5	67.8	414	7	ADE38375		Ade38375 Human pro
16	1325	63.0	419	4	AAB65599		Aab65599 Novel pro
17	1321	62.8	425	4	JAM40592		Aam40592 Human pol
18	1318	62.6	485	5	JAE24141		Aae24141 Human kin
19	1317.5	62.6	384	6	ABU62279		Abu62279 Mouse ser
20	1317.5	62.6	488	5	AAO17709		Aao17709 Murine se
21	1315	62.5	419	4	JAM38806		Aam38806 Human pol
22	1302	61.9	488	6	ABO14992		Abo14992 Human NOV
23	1285.5	61.1	713	5	ABB06090		Abb06090 Human NS
24	1278.5	60.8	399	5	ABB84300		Abb84300 Murine se
25	1259.5	59.9	375	4	AAE04371		Aae04371 Human kin

FT Modified-site 230. .233
 /label= Casein_kinase_II_phosphorylation_site
 PT Modified-site 396
 /label= N_myristoylation_site
 XX PN US2002127683-A1.
 XX PD 12-SEP-2002.
 XX PP 09-MAR-2001; 2001US-00801876.
 XX PR 09-MAR-2001; 2001US-00801876.
 XX PA (YEJJI/) YE J.
 XX PA (YANC/) YAN C.
 XX PA (DPRA/) DI FRANCESCO V.
 XX PA (BEAS/) BEASLEY E M.
 PI Ye J., Yan C., Di Francesco V., Beasley EM;
 XX WPI; 2003-028938/02.
 DR N-PSDB; ABS55499, ABS55500.
 XX PT Novel isolated human kinase peptide useful for treating disorder
 PT characterized by absence of, in appropriate or unwanted expression of the
 kinase protein, and as immunogens to raise antibodies.
 XX PS Claim 1; Fig 2; 174pp; English.
 XX CC The present invention relates to the isolation of a human kinase and the
 CC polynucleotide sequences encoding it. The human kinase of the invention
 CC is related to the serine/threonine kinase subfamily. The gene encoding
 CC the human kinase is located on chromosome 5. The polypeptide and
 CC polynucleotide sequences of the invention are useful for treating a
 CC disease or condition mediated by a human kinase. Both the polypeptide and
 CC polynucleotide sequences are useful as models for the development of
 CC human therapeutics, for identifying therapeutic proteins, as targets for
 CC development of human therapeutic agents, and as query sequences to
 CC perform a search against sequence databases to identify other family
 CC members of related sequences. The polypeptide is useful to raise
 CC antibodies or to elicit another immune response, as a reagent in assays
 CC designed to quantitatively determine levels of the protein in biological
 CC fluids, as markers for tissues in which the corresponding protein is
 CC preferentially expressed, in drug screening assays, in cell-based or cell
 CC -free systems, to identify compounds that modulate kinase activity of the
 CC protein in its natural state, or an altered form that causes the specific
 CC disease or pathology associated with the kinase, to screen a compound for
 CC the ability to stimulate or inhibit interaction between the kinase
 CC protein and a molecule that normally interacts with the kinase protein,
 CC and in pharmacogenomic analysis. The polynucleotide is useful for
 CC monitoring the effectiveness of modulating compounds on the expression or
 CC activity of the human kinase gene in clinical trials or in a treatment
 CC regimen, in diagnostic assays for qualitative changes in a human kinase
 CC nucleic acid that leads to a pathology, for testing an individual for a
 CC genotype that while not necessarily causing a disease, nevertheless
 CC affects the treatment modality, as antisense constructs to control human
 CC kinase gene expression in cells, tissues and organisms, for gene therapy
 CC in patients containing cells that are aberrant in human kinase gene
 CC expression, and to produce transgenic animals. The present sequence
 CC represents a human kinase related to the serine/threonine protein kinase
 CC subfamily
 XX SQ Sequence 396 AA;
 Query Match 100.0%; Score 2104; DB 6; Length 396;
 Best Local Similarity 100.0%; Pred. No. 8.1e-194;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 ERNEVRNVFKELQIMQGLEHPLFLVNLWYSFQDEEDMFMVVDLIGGDLRYHLQQNTHFKB 120
 Qy 121 ETVKLFIGCELVALDYLQNQRIIHRDMKCPDNILLDEGHVHTIDFNIAAMLPRETQITM 180
 Db 121 ETVKLFIGCELVALDYLQNQRIIHRDMKCPDNILLDEGHVHTIDFNIAAMLPRETQITM 180
 Qy 181 AGTKPMAPEMFSSRKKGAGYSFAVDWWSIGVTAYELLRGRPYHRSSTSSKEIVHTFET 240
 Db 181 AGTKPMAPEMFSSRKKGAGYSFAVDWWSIGVTAYELLRGRPYHRSSTSSKEIVHTFET 240
 Qy 241 TVVTPPSAWSQEMVSLLKKLLEPNPDQRFPSOLSVDQNFPPYMDINDAVFQKRLIPGFIP 300
 Db 241 TVVTPPSAWSQEMVSLLKKLLEPNPDQRFPSOLSVDQNFPPYMDINDAVFQKRLIPGFIP 300
 Qy 301 NKGRLNCDPTFELBEMILESKPLHKKKKRLLAKKEKDMRKCDSSOTCLLQEBLDSVQKBPI 360
 Db 301 NKGRLNCDPTFELBEMILESKPLHKKKKRLLAKKEKDMRKCDSSOTCLLQEBLDSVQKBPI 360
 Qy 361 IFNREKVNRDFNKRQPNLALEQTKDPGEDQNNNL 396
 Db 361 IFNREKVNRDFNKRQPNLALEQTKDPGEDQNNNL 396
 RESULT 2
 ID ABU62276 standard; protein; 396 AA.
 XX ABU62276;
 AC AC
 XX DT 01-SEP-2003 (First entry)
 XX DB Human kinase.
 XX KW Human; enzyme; kinase; gene therapy; cancer; inflammation; psoriasis;
 KW arteriosclerosis.
 XX OS Homo sapiens.
 XX PN US2003027307-A1.
 XX PD 06-FEB-2003.
 XX PP 26-SEP-2002; 2002US-00254869.
 XX PR 09-MAR-2001; 2001US-00801876.
 XX PA (APPL-) APPLERA CORP.
 PI Ye J., Yan C., Di Francesco V., Beasley EM;
 XX DR WPI: 2003-492035/58.
 DR N-PSDB; ACA62840, ACA62841.
 XX PT New isolated human kinase proteins, useful for treating disorders
 PT mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis
 PT or psoriasis), or for development of human therapeutics and diagnostic
 PT compositions.
 XX PS Claim 1; Fig 2A; 185pp; English.

CC The invention relates to a new isolated human kinase peptide. The human
 CC kinase peptide and nucleic acid molecules are useful in the development
 CC of human therapeutics and diagnostic compositions. The peptides are
 CC useful for treating disorders (e.g. cancers, inflammations,
 CC arteriosclerosis or psoriasis) characterised by an absence of,
 CC inappropriate, or unwanted expression of the kinase protein. These
 CC molecules are particularly useful as models for developing human
 CC therapeutic targets, identifying therapeutic proteins, or serving as
 CC targets for the development of human therapeutic agents that modulate
 CC kinase activity in cells and tissues that express the kinase. The
 CC peptides are also useful for raising antibodies or eliciting an immune
 CC response; as a reagent (including the labelled reagent) in assays

Query Match 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSGFGEVCIVQKNDTKMCMAMKMNQKCV 60
 Best Local Similarity 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSGFGEVCIVQKNDTKMCMAMKMNQKCV 60
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSGFGEVCIVQKNDTKMCMAMKMNQKCV 60
 Db 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSGFGEVCIVQKNDTKMCMAMKMNQKCV 60
 Qy 61 ERNEVRNVFKELQIMQGLEHPLFLVNLWYSFQDEEDMFMVVDLIGGDLRYHLQQNTHFKB 120

RESULT 4

AAE14261 standard; protein; 396 AA.

ID AAE14261;

XX DT 07-MAR-2002 (First entry)

XX DE Novel human protein (NHP) kinase #4.

XX KW Novel human protein; NHP; gene therapy; diagnosis; drug screening; gene expression; breast cancer; prostate cancer; nutriceutical; cosmetic; medical disorder; mental; biological; physiological; chemotherapeutic.

XX OS Homo sapiens.

XX PN WO200181557-A2.

XX PD 01-NOV-2001.

XX PP 24-APR-2001; 2001WO-US013149.

XX PR 25-APR-2000; 2000US-0199499P.

PR 01-MAY-2000; 2000US-0201227P.

XX PA (LEXI-) LEXICON GENETICS INC.

PI Hu Y, Nepomnych B, Wang X, Donoho G, Scoville J, Walko DW; XX WPI; 2002-034442/04.

DR N-PSDB; AAD23679.

XX PT New nucleic acid molecules encoding new human proteins, useful in diagnosis, drug screening, clinical trial monitoring, treatment of physiological disorders, and cosmetic or nutriceutical applications.

PT PT

PT PS Claim 7; Page 43; 44pp; English.

XX CC The invention relates to novel human protein (NHP) kinases and their corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as pharmaceutical and medical reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. NHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or diseases, and cosmetic and nutriceutical applications. NHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular chromosome. NHP DNA is further useful as hybridisation probes for screening libraries and assessing gene expression patterns, and also for the detection of mutant NHPs or inappropriately expressed NHPs for disease diagnosis. NHP DNA is also useful in gene therapy. The present sequence is novel human protein (NHP) kinase which is similar to serine/threonine protein kinases, ribosomal protein kinases and cAMP-dependent kinases related to the invention.

XX SQ Sequence 396 AA;

Query Match 99.3%; Score 2089; DB 5; Length 396;

Best Local Similarity 99.5%; Pred. No. 2.3e-192;

Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVFDENEDVNPDHPEILRAIGKGSFGEVCIVQKNDTKKOMCAMKYMNKQKCV 60

Db 1 MGANTSRKPPVFDENEDVNPDHPEILRAIGKGSFGEVCIVQKNDTKKOMCAMKYMNKQKCV 60

QY 61 ERNEVRNVPKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDDLLGGDLRYHLQQNTHFK 120

Db 61 ERNEVRNVPKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDDLLGGDLRYHLQQNTHFK 120

QY 121 ETVKLPLICELVMALDYLQNQRRIIHDMKPDNILLDEHGHVHTDFNIAAMLPRETQITM 180

Db 121 ETVKLPLICELVMALDYLQNQRRIIHDMKPDNILLDEHGHVHTDFNIAAMLPRETQITM 180

XX DR WPI; 2002-329769/36.

QY 181 AGTKPYMAPEMFSSRKGAGYSFAVDWWSLGVVTAYELLRGRRPYHRSSTSKEIVVHTFET 240

Db 181 AGTKPYMAPEMFSSRKGAGYSFAVDWWSLGVVTAYELLRGRRPYHRSSTSKEIVVHTFET 240

AC 241 TVVTPSAWSQEMVSLLKKLLEPNPQDFSQLSDVQNFPMNDINWDAVFQKRLLPGFIP 300

Db 241 TVVTPSAWSQEMVSLLKKLLEPNPQDFSQLSDVQNFPMNDINWDAVFQKRLLPGFIP 300

DE 301 NKGRLNCDPTFELEMILESKPLHKKKKRLAKKEKDMLRKCDSSQTCLLQEHLDSVQKEIFI 360

Db 301 NKGRLNCDPTFELEMILESKPLHKKKKRLAKKEKDMLRKCDSSQTCLLQEHLDSVQKEIFI 360

OS 361 IFNREKVNRDFNQKQPNLALLEQTKDQGEGDQNNNL 396

Db 361 IFNREKVNRDFNQKQPNLALLEQTKDQGEGDQNNNL 396

RESULT 5

AAE21725

ID AAE21725 standard; protein; 396 AA.

XX AC AAE21725;

XX DT 16-JUL-2002 (First entry)

XX DE Human PKIN-20 protein.

XX KW Human; kinase; enzyme; PKIN-20 protein; immune system disorder; anaemia; acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease; asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease; AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder; Down's syndrome; gene therapy; protein therapy; cytostatic.

XX OS Homo sapiens.

XX FH Key Domain

FT FT /note= "Protein kinase domain"

FT FT /note= "Protein kinase domain"

FT FT /note= "Protein kinase domain"

FT FT /note= "Eukaryotic protein kinase domain"

FT FT /note= "Protein kinase domain"

XX PR WO200218557-A2.

XX PD 07-MAR-2002.

XX PP 31-AUG-2001; 2001WO-US027219.

XX PR 31-AUG-2000; 2000US-0229873P.

PR 08-SEP-2000; 2000US-0231357P.

PR 14-SEP-2000; 2000US-0232654P.

PR 22-SEP-2000; 2000US-0234902P.

PR 29-SEP-2000; 2000US-0236499P.

PR 06-OCT-2000; 2000US-0238389P.

PR 13-OCT-2000; 2000US-0240542P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Bandman O, Nguyen DB, Wallia NK, Hafalia AJA, Yao MG, Gandhi AR, Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM, Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT, Azimzai Y, Burkill JD, Marcus GA, Zingler KA, Lu DAM, Lai PG, Ramkumar J, Warren BA, Kearney L, Policky JL, Thangavelu K, Burford N;

XX DR WPI; 2002-329769/36.

DR N-PSDB; AAD34317.
 XX New human kinases, useful for diagnosing, treating or preventing immune system disorders (e.g. Crohn's disease), neurological disorders (e.g. epilepsy), or cell proliferative disorders (e.g. cancers such as leukemia or lymphoma).

XX Claim 75; Page 184-185; 218pp; English.

CC The present invention relates to human kinases (PKIN) and polynucleotides encoding such proteins. PKIN sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of PKIN, particularly immune system disorders (e.g. acquired immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease, anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-Tooth disease or seizures), cell proliferative disorders (e.g. cancers such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma), and developmental disorders (e.g. Down's syndrome). They are also used in gene therapy and protein therapy. The present sequence is human PKIN-20 protein

XX Sequence 396 AA;

SQ Query Match 99.3%; Score 2089; DB 5; Length 396;

Best Local Similarity 99.5%; Pred. No. 2.3e-192; Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEBVCIYQNDTTRKMCAMKYMNNKQKCV 60
 Db 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGKVCIYQNDTTRKMYAMKYMNNKQKCV 60
 Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVYDLLGGDLRYHLQQNVHFKE 120
 Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVYDLLGGDLRYHLQQNVHFKE 120
 Qy 121 ETVKLIFICBLVMA LDYLQNQRRIIHRDMKPDNILLDEHGHYHITDENIAAMLPREQTITM 180
 Db 121 ETVKLIFICBLVMA LDYLQNORIIIHRDMKPDNILLDEHGHYHITDENIAAMLPREQTITM 180
 Qy 181 AGTKP YMAPEMFSSRKGAGYSFAVDWWSLGVTA YBLLRGRPRPHIRSSTS SKBIVHTFET 240
 Db 181 AGTKP YMAPEMFSSRKGAGYSFAVDWWSLGVTA YBLLRGRPRPHIRSSTS SKBIVHTFET 240
 Qy 241 TVVTYPSAWSQEMVSLLKKCLEPNPDQRFSQLSDVQNFPMNDINWDAFQKR LIPGFIP 300
 Db 241 TVVTYPSAWSQEMVSLLKKCLEPNPDQRFSQLSDVQNFPMNDINWDAFQKR LIPGFIP 300
 Qy 301 NKGRLNCDPTFELLEMILESKPLHKKKKRLAKKEKD MRKCDSSOTCLQEHLD SVQKEFI 360
 Db 301 NKGRLNCDPTFELLEMILESKPLHKKKKRLAKKEKD MRKCDSSOTCLQEHLD SVQKEFI 360
 Qy 361 IFNREKVNRDENKRPQNLALEQTKD PQGEDQNNL 396
 Db 361 IFNREKVNRDENKRPQNLALEQTKD PQGEDQNNL 396

RESULT 6
 ID AAM50334 standard: protein; 396 AA.

XX AAM50334;

XX DT 04-FEB-2002 (first entry)

XX DE Human 14911 protein kinase.

XX KW Protein kinase; human; signal transduction; lung cancer; colon cancer; brain cancer; breast cancer; therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers 2. .7
 FT Modified-site

FT PT Modified-site /note= "N-myristoylated"
 PT PT Modified-site /note= "ASN is N-glycosylated"
 PT PT Modified-site 5. .7 /note= "O-phosphorylated by protein kinase C"
 PT Domain 23. .281 /label= Protein_kinase_domain
 PT Peptide 29. .37 /note= "protein kinase ATP-binding region signature"
 PT PT Modified-site 43. .46 /note= "protein kinase ATP-binding region signature"
 PT PT Modified-site 45. .47 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 89. .92 /note= "O-phosphorylated by casein kinase II"
 PT PT Modified-site 122. .124 /note= "O-phosphorylated by protein kinase C"
 PT Active-site 142. .154 /note= "active site signal"
 PT PT Modified-site 193. .195 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 197. .202 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 212. .215 /note= "O-phosphorylated by casein kinase II"
 PT PT Modified-site 218. .221 /note= "Amidated"
 PT PT Modified-site 230. .233 /note= "O-phosphorylated by casein kinase II"
 PT PT Modified-site 230. .232 /note= "O-phosphorylated by protein kinase C"
 PT Domain 282. .301 /label= Protein_kinase_C-terminal_domain
 PT PT Modified-site 391. .396 /note= "N-myristoylated"
 PT PT Modified-site 392. .397 /note= "N-myristoylated"
 PT PT Modified-site 400. .401 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 406. .407 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 412. .413 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 418. .419 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 424. .425 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 430. .431 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 436. .437 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 442. .443 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 448. .449 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 454. .455 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 460. .461 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 466. .467 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 472. .473 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 478. .479 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 484. .485 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 490. .491 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 496. .497 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 502. .503 /note= "O-phosphorylated by protein kinase C"
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 PT PT Modified-site 514. .515 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 520. .521 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 526. .527 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 532. .533 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 538. .539 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 544. .545 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 550. .551 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 556. .557 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 562. .563 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 568. .569 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 574. .575 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 580. .581 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 586. .587 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 592. .593 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 598. .599 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 604. .605 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 610. .611 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 616. .617 /note= "O-phosphorylated by protein kinase C"
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 PT PT Modified-site 694. .695 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 698. .699 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 704. .705 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 710. .711 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 716. .717 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 722. .723 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 728. .729 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 734. .735 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 740. .741 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 746. .747 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 752. .753 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 758. .759 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 764. .765 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 770. .771 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 776. .777 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 782. .783 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 788. .789 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 794. .795 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 800. .801 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 806. .807 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 812. .813 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 818. .819 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 824. .825 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 830. .831 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 836. .837 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 842. .843 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 848. .849 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 854. .855 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 860. .861 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 866. .867 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 872. .873 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 878. .879 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 884. .885 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 890. .891 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 896. .897 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 902. .903 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 908. .909 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 914. .915 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 920. .921 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 926. .927 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 932. .933 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 938. .939 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 944. .945 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 950. .951 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 956. .957 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 962. .963 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 968. .969 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 974. .975 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 980. .981 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 986. .987 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 992. .993 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 998. .999 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1004. .1005 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1010. .1011 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1016. .1017 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1022. .1023 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1028. .1029 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1034. .1035 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1040. .1041 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1046. .1047 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1052. .1053 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1058. .1059 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1064. .1065 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1070. .1071 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1076. .1077 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1082. .1083 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1088. .1089 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1094. .1095 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1100. .1101 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1106. .1107 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1112. .1113 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1118. .1119 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1124. .1125 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1130. .1131 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1136. .1137 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1142. .1143 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1148. .1149 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1154. .1155 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1160. .1161 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1166. .1167 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1172. .1173 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1178. .1179 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1184. .1185 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1190. .1191 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1196. .1197 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1202. .1203 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1208. .1209 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1214. .1215 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1220. .1221 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1226. .1227 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1232. .1233 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1238. .1239 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1244. .1245 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1250. .1251 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1256. .1257 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1262. .1263 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1268. .1269 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1274. .1275 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1280. .1281 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1286. .1287 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1292. .1293 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1298. .1299 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1304. .1305 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1310. .1311 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1316. .1317 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1322. .1323 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1328. .1329 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1334. .1335 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1340. .1341 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1346. .1347 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1352. .1353 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1358. .1359 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1364. .1365 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1370. .1371 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1376. .1377 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1382. .1383 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1388. .1389 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1394. .1395 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1400. .1401 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1406. .1407 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1412. .1413 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1418. .1419 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1424. .1425 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1430. .1431 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1436. .1437 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1442. .1443 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1448. .1449 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1454. .1455 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1460. .1461 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1466. .1467 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1472. .1473 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1478. .1479 /note= "O-phosphorylated by protein kinase C"
 PT PT Modified-site 1484. .1485 /note= "O-phosphorylated by protein kinase C"
 PT PT

CC a cellular proliferation and/or differentiation disorder, especially lung, colon, brain and breast cancer, a small molecule, peptide, phosphopeptide, anti-14911 antibody, a 14911 polypeptide or its variant.. Other disorders that may be diagnosed/treated include those associated with bone metabolism, autoimmune diseases, cardiovascular disorders, liver disorders, viral diseases, pain and metabolic disorders

XX Sequence 396 AA;

Query Match 99.0%; Score 2083; DB 5; Length 396;

Best Local Similarity 99.2%; Pred. No. 8.6e-192; Matches 393; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGANTSRSRKPPVFDENEDVNFDHFBIILRAIGKGSFGBVCIVQNDTKKMCAMKYMNKQKCV 60

Db 1 MGANTSRSRKPPVFDENEDVNFDHFBIILRAIGKGSFGBVCIVQNDTKKMCAMKYMNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDDMFMVVDLILLGGDLRYHLQQNYHFKB 120

Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDDMFMVVDLILLGGDLRYHLQQNYHFKB 120

Qy 121 ETVKLIFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITM 180

Db 121 ETVKLIFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITM 180

Qy 181 AGTRKPYMAPEMFSSRKGAGYSFAVDWWNSLGVTAYELLGRGRRPYHRSSTSSKERVTFET 240

Db 181 AGTRKPYMAPEMFSSRKGAGYSFAVDWWNSLGVTAYELLGRGRRPYHRSSTSSKERVTFET 240

Qy 241 TVVTPPSAWSQEMVSLLKKLLEPQRPSQLSDVQNFPMNDINWDAYPQRKLIPGPPIP 300

Db 241 TVVTPPSAWSQEMVSLLKKLLEPQRPSQLSDVQNFPMNDINWDAYPQRKLIPGPPIP 300

Qy 301 NKGRLNCDPTFELEEMILESKPLHKKKKRLAKKEKDMRKCDSROTCLLQEHLDSVQKEFI 360

Db 301 NKGRLNCDPTFELEEMILESKPLHKKKKRLAKKEKDMRKCDSROTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNDRFNKRQPNLALEQTKDPOGEDQNNNL 396

Db 361 IFNREKVNDRFNKRQPNLALEQTKDPOGEDQNNNL 396

Qy 7 AAE14260 standard; protein; 407 AA.

DB 07-MAR-2002 (first entry)

XX Novel human protein (NHP) kinase #3.

XX Novel human protein; NHP; gene therapy; diagnosis; drug screening; gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic; medical disorder; mental; biological; physiological; chemotherapeutic.

XX OS Homo sapiens.

XX PN WO200181557-A2.

XX PD 01-NOV-2001.

XX PF 24-APR-2001; 2001WO-US013149.

XX PR 25-APR-2000; 2000US-0199499P.

XX PR 01-MAY-2000; 2000US-0201227P.

XX (LEXI-) LEXICON GENETICS INC.

XX Hu Y, Nepomnych B, Wang X, Donoho G, Scoville J, Walke DW;

XX DR WPI; 2002-034442/04.

DR N-PSDB, ADD23678.

XX Human protein kinase #4.

XX ID AAU03504 standard; protein; 327 AA.

XX AC AAU03504;

XX DT 12-SEP-2001 (first entry)

XX DE Human protein kinase #4.

XX RESULT 8

XX AAU03504

XX ID AAU03504

XX AC AAU03504;

XX DT 12-SEP-2001 (first entry)

XX DE Human protein kinase #4.

XX KW Human; Protein kinase; PTK; cancer; cardiovascular disease;

KW metabolic disorder; immune related disease; neurological disorder;

KW neurodegenerative disorder; inflammatory disorder; infectious disease;

KW KW

KW reproductive disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200138503-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032085.
 XX
 PR 24-NOV-1999; 99US-0167482P.
 XX
 PA (SUGE-) SUGEN INC.
 XX
 PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Planagan P, Clary D;
 XX
 DR 2001-343950/36.
 XX
 DR N-PSDB; AAS06704.
 XX
 PT Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX
 PS Claim 7; Fig 2; 433pp; English.
 XX
 CC AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate kinase expression. For example, they may be used to treat
 CC cancers (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be used for
 CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
 CC polypeptides may be used as antigens in the production of antibodies
 CC against the protein kinases and in assays to identify modulators of
 CC protein kinase expression and activity
 XX
 SQ Sequence 327 AA;
 Query Match 71.3%; Score 1500.5; DB 4; Length 327;
 Best Local Similarity 87.0%; Pred. No. 9.1e-136;
 Matches 295; Conservative 6; Mismatches 19; Indels 19; Gaps 4;
 Qy 1 MGANTSRKPPFPFDENEDVNFDHPEILRAIGKGSFGBVCIVQKNDTKRMCAKTMNKQKCV 60
 Db 1 MGANTSRKPPFPFDENEDVNFDHPEILRAIGKGSFGBVCIVQKNDTKRMCAKTMNKQKCV 60
 Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMVYDLLGGDLRYLQONVHFKE 120
 Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMVYDLLGGDLRYLQONVHFKE 120
 SQ Sequence 404 AA;
 Query Match 67.8%; Score 1427; DB 6; Length 404;
 Best Local Similarity 69.5%; Pred. No. 1.5e-128;
 Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;
 Qy 1 MGANTSRKPPFPFDENEDVNFDHPEILRAIGKGSFGEVICVQKNDTKRMCAKTMNKQKCV 60
 Db 1 MGGNHSKPPFPFDENEDVNFDHPEILRAIGKGSFPGKVIVQKRDTKRMCAKTMNKQKCV 60
 Qy 121 ETVKLIFICELVMDYLNQNRRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITM 180
 Db 121 ETVKLIFICELVMDYLNQNRRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITM 180
 Qy 181 AGTKPYPMAPEMFSSRKGAGYSFAVDWNSLGVTAYELLRGRRPYHRSSTSKEIVHTFET 240
 Db 181 AGTKPYPMAPEMFSSRKGAGYSFAVDWNSLGVTAYELLRGRRPYHRSSTSKEIVHTFET 240
 Qy 241 TVVTPSAWSQEMVSLKKLLE---PNPDQRFSQLSDVQ---NFPYMANDINWDAVFQKR 293
 Db 241 TVVTPSAWSQEMVSLKKVRRKTACPNEVTKGSRSLGSLSLEVIQY---WGHQLSSL 295
 Qy 294 LIPGPPIPKNKGRLNCDPTELEEMILESKPLHKKKKRKLAK 332
 Db 296 -----QKGRINCDPTFBLEEMILESKPLHKKKKRKLAK 327

Db	121	EGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHIGHVHTIDFNIAITVLKGSEKASS	180	XX	Sequence 403 AA;
Qy	180	MAGTKPMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLOWLLRGRPYHIIRSSSTSSKEIVHT	237	SQ	Score 1425.5; DB 6; Length 403;
Db	181	MAGTKPMAPEVQYVNDGPGYSYSPDWSLGVTAYELLOWLLRGRPYEIHSATPIDELNM	240	Query Match 67.8%; Best Local Similarity 68.2%; Pred. No. 2.1e-128; Mismatches 77; Indels 7; Gaps 3;	
Qy	238	FETTVVTPPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDDINWDAVPQKRRLPG	297	Qy	1 MGANTSRKPPVFDENEDVNFDHPEILRAIGKGSFGEVCIVQKNDTKKMCAMKYMANKQKCV 60
Db	241	FKVERVHYSSSTWCAGMSLKLKQLTQDPESRLLSLRDIQSMTYLAADMNWDAVFEKALMPG	300	Db	1 MGGNHSHKPKPPVFDENEEVNFDHFOILRAIGKGSFGEVCIVQKNDTKKMYAMKYMANKQKCI 60
Qy	298	PIPNAKGRLNCDETPFBLEMILESKPLHKKKKRLLAK-KEKDMRKCDSSQTCLLQEHLLDSVQ	356	Qy	61 ERNEVRNVYFKELQIMQGLEHPFLVNLWYSQDFEDMFMVVDLILLGGDLRYHLQONVHFKE 120
Db	301	FVVPNKGRLNCDETPELEEMILESKPLHKKKKRLLAKHRSRDSTKDSCPLNGLHQOCLETVR	360	Db	61 ERDEVNVYFRELQIMQGLEHPFLVNLWYSQDFEDMFMVVDLILLGGDLRYHLQONVHFTE 120
Qy	357	KEFIIFNRERKVNRDFDNKRPQPNLALEQTKDPOGEDGQNNNL	396	Qy	121 ETVKLPICBLVMALDYLQNLQRRIHRDMKPDNILLDEHIGHVHTIDFNIAAMLPRETOQTITM 180
Db	361	KEFIIFNRERKLRQ-----QGDGQLSDL	384	Db	121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHIGHVHTIDFNIAVTVKGAERASSM 180
<hr/>					
RESULT 10					
ABU62278	ID	ABU62278 standard; protein; 403 AA.	XX	Qy	181 AGTKPYNMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLOWLLRGRPYHIIRSSSTSSKEIVHTF 238
AC	XX	ABU62278;	AC	Db	181 AGTKPYNMAPEVFQVYMDRGPGYSYSPDWSLGLITAYELLRGWRPYBHSVTPIDEILNMF 240
DT	XX	01-SEP-2003 (first entry)	Qy	239 BTVVVTYPSAWSQEMVSLLKKLLEPQLNPQDFRSQLSDQNFPYMNDDINWDAVPQKRRLPGF 298	
XX	XX	Human serine/threonine protein kinase #1.	Db	241 KVERVHYSSSTWCKGMVALLRKLLTDPESRVSSLHDIQSVPLADMNWDAVFKKALMPGF 300	
DB	XX	Human; enzyme; kinase; gene therapy; cancer; inflammation; psoriasis; arteriosclerosis.	Qy	299 IPNKGRLNCDPTFBLREMILESKPLHKKKKRLLAK-KEIKDMRKCDSSQTCLLQEHLLDSVQK 357	
KW	XX	OS Homo sapiens.	Db	301 VPKNGRLNCDTPTFBLREMILESKPLHKKKKRLLAKNRSRDGTxDSCPLNGLHQCHLETRB 360	
KW	XX	PN US2003027307-A1.	Qy	358 BFILLENREKVNRDFNKRQPNLIALEQTKDPOQ---EDGQNNNL 396	
OS	XX	PD 06-FEB-2003.	Db	361 EPIIPNREKLRQQGGSQULLTDSRGGQAQSKLQDGNNNL 403	
<hr/>					
RESULT 11					
		AAB65600	XX	XX	XX Human; mouse; protein kinase; antiarthritic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
		ID AAB65600 standard; protein; 414 AA.	AC	AC AAB65600;	XX
		XX	XX	XX	DT 27-MAR-2001 (first entry)
		XX	XX	XX	DE Novel protein kinase, SEQ ID NO: 125.
		XX	XX	XX	XX OS Homo sapiens.
		XX	XX	XX	XX PN WO200073469-A2.
		PP 26-SEP-2002; 2002US-00254869.	XX	XX	XX PD 07-DEC-2000.
		PR 09-MAR-2001; 2001US-000801876.	XX	XX	XX PP 26-MAY-2000; 2000WO-US014842.
		XX PA (APPL-) APPLERA CORP.	XX	XX	XX PR 28-MAY-1999; 99US-0136503P.
		XX PI Ye J., Yan C., Di Francesco V., Beasley EM;	XX	XX	XX PA (SUGE-) SUGEN INC.
		XX DR WPI; 2003-492035/58.	XX	XX	XX PN Plowman GD, Martinez R., Whyte D, Sudersanam S;
		XX PR 2001-032161/04.	XX	XX	XX DR N-PSDB, AAP44625.
		CC The invention relates to a new isolated human kinase peptide. The human kinase peptide and nucleic acid molecules are useful in the development of human therapeutics and diagnostic compositions. The peptides are useful for treating disorders (e.g. cancers, inflammations, arteriosclerosis or psoriasis) characterised by an absence of, inappropriate, or unwanted expression of the kinase protein. These molecules are particularly useful as models for developing human therapeutic targets, identifying therapeutic proteins, or serving as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The peptides are also useful for raising antibodies or eliciting an immune response; as a reagent (including the labelled reagent) in assays designed to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids; or as markers for tissues in which the corresponding protein is preferentially expressed. The agents identified are useful for treating a subject with a disorder mediated by kinase pathway. The present sequence represents the amino acid sequence of the human serine/threonine protein kinase #1	CC	CC	CC Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers.

RESULT 13
AAO17710 standard; protein; 414 AA.
ID AAO17710;
XX
AC
XX
DT 20-AUG-2002 (first entry)
XX
DE Human serine-threonine protein kinase #2.
XX
KW Human; serine-threonine protein kinase; cancer; diabetes; obesity; central nervous system disorder; inflammation; gene therapy; COPD; neuroprotective; antiparkinsonian; cerebroprotective; cytostatic; antidiabetic; antiallergic; antiasthmatic; antidepressant; anorectic; antiinflammatory; immunomodulator; chronic obstructive pulmonary disease; enzyme.
XX
OS Homo sapiens.
XX
PN WO200233056-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-EP011892.
XX
PR 16-OCT-2000; 2000US-0240097P.
XX
PR 30-JUL-2001; 2001US-0308096P.
(FARB) BAYER AG.
XX
PA
XX
PT Koehler RH;
XX
DR WPI; 2002-435534/46.
XX
PT New human serine-threonine protein kinase and encoding polynucleotides, useful for diagnosing, treating and preventing central nervous system disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).
XX
PS Disclosure; Fig 8; 135pp; English.
XX
CC The present invention provides the protein and coding sequences of a human serine-threonine protein kinase. The sequences can be used in the diagnosis, treatment and prevention of cancers (e.g. leukaemia, lymphoma or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or traumatic brain injury), diabetes, eating disorders (e.g. obesity, anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and chronic obstructive pulmonary disease (COPD). The present sequence is a human serine-threonine protein kinase.
XX
SQ Sequence 414 AA;

Query Match	67.8%	Score 1425.5;	DB 5;	Length 414;
Best Local Similarity	68.2%	Pred. No. 2.2e-128;		
Matches 275; Conservative	44;	Mismatches 77;	Indels 7;	Gaps 3;

Qy 1 MGANTSRKPPVFDENEDVNFDHFBILRAIGKGSFGVBIVQKNDTKMCMAMKYMNRKCV 60
Db 1 MGGNHSKPPVFDENEEVNFDHFQIILRAIGKGSFGKVIVQKRDTKMAMKYMNRKCI 60
Qy 61 ERNEVRANVFKELQIMQGLSHPPFLVNLWYSFQDDEDMDMFVVDLILGGDLRYHLQONVHPKE 120
Db 61 ERDEVANVFRFLQIMQGLEHPPFLVNLWYSFQDDEDMDMFVVDLILGGDLRYHLQONVHFTE 120
Qy 121 ETVKLPICELVMALDYLQNRTHIHDMKPDNTILLDEHGHVHTDFNTIAAMLPRBTQITTM 180
Db 121 GTVKLYICELAALLEYLQRYHIHDRIKPDNILLDEHGHVHTDFNTIAVVKGAERASSM 180
Qy 181 AGTKPVMAPEMS--SRKGAGYSFAVDWWMSLGTAYELLRGRRPYHRSSTSSKRIVHTTF 238
Db 181 AGTKPVMAPEVQVYMDRGPGYSYPVDDWSLGITAYELLRGWRPYEIHSSVTPIDEBILNMF 240
Qy 239 ETTVVTTPSAWSQEMVSLLKKLEPNPFDQRFSQLSDVQNFFYMDINWDAVFQKRLLJPGF 298

RESULTS 14
ABR58617
ID ABR58617 standard; protein; 414 AA.
XX
DE Human cancer related protein SEQ ID NO:274.
XX
XX
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
PN WO2003025138-A2.
XX
PD 27-MAR-2003.
XX
PP 17-SEP-2002; 2002WO-US029560.
XX
PR 17-SEP-2001; 2001US-0323469P.
PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PT Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KB;
PI PI Zlotnik A;
XX
DR WPI; 2003-354600/33.
DR N-PSDB; ACC72764.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 748; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in drug screening, particularly for identifying agents for treating these

CC pathologies
 XX Sequence 414 AA;
 SQ Query Match 67.8%; Score 1425.5; DB 6; Length 414;
 Best Local Similarity 68.2%; Pred. No. 2.2e-128;
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 Qy 358 EPIIFNREKVNDPDKQPNLALEQTKDPOG---EDGQNNNL 396
 Db 361 EPIIFNREKVCLRRQQGQGSQULLDTDSRGGGQAQSKLQDGCGNNNL 403

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 XX AC ADE38375;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human protein 3703 amino acid sequence.
 XX WO2003065006-A2.
 XX PD 07-AUG-2003.
 XX PP 30-JAN-2003; 2003WO-US002588.

XX PR 31-JAN-2002; 2002US-0353600P.
 PR 15-MAR-2002; 2002US-0364517P.
 PR 09-APR-2002; 2002US-0371075P.
 PR 10-APR-2002; 2002US-0371507P.
 PR 16-APR-2002; 2002US-0372984P.
 PR 19-APR-2002; 2002US-0374194P.
 PR 24-MAY-2002; 2002US-0382995P.
 PR 31-MAY-2002; 2002US-0385023P.
 PR 14-JUN-2002; 2002US-0388853P.
 PR 17-JUN-2002; 2002US-0389395P.
 PR 25-JUN-2002; 2002US-0391324P.
 PR 15-JUL-2002; 2002US-0395944P.
 PR 22-JUL-2002; 2002US-0397726P.

PA PR 13-AUG-2002; 2002US-0403046P.
 PR 22-AUG-2002; 2002US-0405155P.
 PR 27-AUG-2002; 2002US-0406361P.
 PR 25-OCT-2002; 2002US-0421195P.
 PR 12-NOV-2002; 2002US-0425456P.
 PR 19-NOV-2002; 2002US-0427626P.
 PR 10-DEC-2002; 2002US-0432122P.
 XX PA (MILL-) MILLENIUM PHARM INC.
 XX AX Hunter JJ, Macbeth KJ, Tsai F, Lesson A, Lightcap ES;
 PI PI Williamson MW, Rudolph-Owen LA;
 XX XX DR N-PSDB; ADE38374.
 XX PT Treating subject having tumorigenic disorder or angiogenic disorder caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic acid, by administering a modulator.
 XX PS Disclosure; SEQ ID NO 36; 454pp; English.
 XX XX DR N-PSDB; ADE38374.
 XX PT This invention relates to a novel method of treating a human subject having a tumorigenic disorder or angiogenic disorder, caused by aberrant gene expression or activity of an isolated protein, by administering a modulator. The modulator may have cytostatic, antithyroid, antidiabetic or ophthalmological activity. The method is useful for treating a subject having a tumorigenic or angiogenic disorder, in particular for treating cancer (for example breast cancer, colon cancer or prostate cancer) and, for example, Grave's disease and diabetic retinopathy. The present sequence is the amino acid sequence of the novel isolated human protein 3703 of the invention.
 XX SQ Sequence 414 AA;
 XX Query Match 67.8%; Score 1425.5; DB 7; Length 414;
 Best Local Similarity 68.2%; Pred. No. 2.2e-128;
 Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

Qy 1 MGANTSRKPPVFDENEDVNFDHFETILRAIGKGSFGEVCIVQKNDTKMCMAMKYMNKQKCV 60
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 Db 121 GTVKLYICELALLEYLQRYHIIRARDIKPDNPNTLLDEHGHVHITDENTIAATVKGABRASSM 180
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 Db 241 KVERVHYSSTWCKGMVALRKKLLTDPESRVSSLHDIOSVPYLAADMNWDAFKKALMPGF 300
 Qy 299 IPNKGRLNCDPTELEEMILESPLHKKKKRLLAK-KEKDMRKCDSSQTCLLQEHLDSVQK 357
 Db 301 VPKNGRLNCDPTELEEMILESPLHKKKKRLLAKNSRSRGTKDSCPLNGLHQCLETVRE 360
 Qy 358 EPIIFNREKVNDPDKQPNLALEQTKDPOG---EDGQNNNL 396
 Db 361 EPIIFNREKVCLRRQQGQGSQULLDTDSRGGGQAQSKLQDGCGNNNL 403

Qy 121 ETVKLFIGELYMAODYLQLNQRLIIRDMKRPDNNTLLDEHGHVHITDENTIAAMLPRETQITTM 180
 Db 121 GTVKLYICELALLEYLQRYHIIRARDIKPDNPNTLLDEHGHVHITDENTIAATVKGABRASSM 180
 Qy 61 ERNEVRNVFKELOIIMQGLEHPPFLVNLWYSFQDDEEDMFMVVDLILLGGDLRHLQQNVBFKE 120
 Db 61 ERDEVRNVFRELQIMQGLEHPPFLVNLWYSFQDDEEDMFMVVDLILLGGDLRHLQQNVBFKE 120
 Qy 121 ETVKLFIGELYMAODYLQLNQRLIIRDMKRPDNNTLLDEHGHVHITDENTIAAMLPRETQITTM 180
 Db 121 GTVKLYICELALLEYLQRYHIIRARDIKPDNPNTLLDEHGHVHITDENTIAATVKGABRASSM 180
 Qy 181 AGTKPYPAMEMFS--SRKGAGYSFAVDWWWSLGVTAYELLGRGPYHIRSTSSSKBIVHTP 238
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 Db 241 KVERVHYSSTWCKGMVALRKKLLTDPESRVSSLHDIOSVPYLAADMNWDAFKKALMPGF 300
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 Db 301 VPKNGRLNCDPTELEEMILESPLHKKKKRLLAKNSRSRGTKDSCPLNGLHQCLETVRE 360
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 Db 361 EPIIFNREKVCLRRQQGQGSQULLDTDSRGGGQAQSKLQDGCGNNNL 403

Search completed: June 25, 2004, 10:49:07
 Job time : 62 secS

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 20:55:12 ; Search time 2826 Seconds
 (without alignments)
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Title: US-10-667-442-1

Perfect Score: 1485

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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB Seq length: 0

Maximum DB Seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

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8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gbs_hum:*

18: em_gbs_inv:*

19: em_gbs_pln:*

20: em_gbs_vrt:*

21: em_gbs_fun:*

22: em_gbs_mam:*

23: em_gbs_mus:*

24: em_gbs_pro:*

25: em_gbs_rod:*

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28: gb_gbs1:*

29: gb_gbs2:*

Result No.	Score	Query	Match	Length	DB ID	Description
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2	968	65.2	2477	11	AK044474	AK044474 Mus muscu
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4	710.6	47.9	893	10	BG036777	BG036777 602286992

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	968	65.2	1927	11	AK042599	AK042599 Mus muscu
2	968	65.2	2477	11	AK044474	AK044474 Mus muscu
3	968	65.2	3766	11	AK036266	AK036266 Mus muscu
4	710.6	47.9	893	10	BG036777	BG036777 602286992

1	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Carninci, P. and Hayashizaki, Y.
2	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	High-efficiency full-length cDNA cloning
3	Genome Res. 10 (10), 1617-1630 (2000)	Meth. Enzymol. 303, 19-44 (1999)
4	20499374	1
5	11042159	2

Qy	901	CTAATAAGCAGGTGAATTGTGATCCCTTGAACCTGGAAATGATTGGAGT	960	REFERENCE AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitamura, T., Tashiro, H., Ito, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishimura, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kiria, A. and Hayashizaki, Y.
Db	1254	CGACCAAAGGCAACTTCAATTGTGACCCCACTTTGAAGAAATGATTGGAGT	1313	DEFINITION	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Qy	961	CCAAACCTCTACAATAAGAAAAAGGGCTGGCAAAAGGAAGGATATGAGGAAT	1020	TITLE	Genome Res. 10 (11), 1757-1771 (2000)
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Qy	1021	GCGATTCTTCAGACATGTCTTCAAGAGCACTTGACTCTGTCCAGAAGGAGTCA	1080	REFERENCE AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Db	1374	GTGACTCCCTCTCACAGACGTGCTTCAAGAGCATCTTGATGCTGTTCAAGAAGAATTAA	1433	TITLE JOURNAL MEDLINE PUBMED	Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Nature 420, 563-573 (2002)
Qy	1081	TAATTTCACAGAGAAAAAGTAAACAGGACTTTAACAAACCAATCTAGCCT	1140	REFERENCE AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Db	1434	TAATTTCACAGAGAAAAGTAAAGTAAAGTACTTAACTCAGAGAACAAATCTAGCCT	1493	TITLE JOURNAL MEDLINE PUBMED	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs (bases 1 to 2477) Nature 420, 563-573 (2002)
Qy	1141	TGGAACAAACCAAAAGAC-----CCACAAACACACAGAGGAGGAGGCCAGAA	1194	REFERENCE AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Ohno, M., Ohnatio, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Db	1494	TGGAACAAACACAGAGGAGGAGGCCAGAA	1553	TITLE JOURNAL MEDLINE PUBMED	Direct Submission
Qy	1195	GGCCTCATG-----TCTCTCTCTTGGGACAAT-----CTATGCCAGAAA	1234	COMMENT	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
Db	1554	GTGCTCCGAGTCCTGGGGACAGTGGTCTGGGACACTGGTCTGGGAA	1613	TITLE JOURNAL MEDLINE PUBMED	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genomic Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Qy	1235	CTTCTTAATTACATATGTCAAGAAAGCTGACAGTAGCTCTGCCACT-CCACACCCATG	1293	DEFINITION	Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.
Db	1614	AGTCCCTGATTATCACACACAGAGCTGACAGGAGTCCCTGGCAACACCTCTATG	1673	COMMENT	URL: http://genome.gsc.riken.go.jp/ http://fantom.gsc.riken.go.jp/ http://organism="Mus musculus" /mol type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM DB:A930015B13" /db_xref="MGI:2409788" /clone="A930015B13" /tissue type="retina" /clone lib="RIKEN full-length enriched mouse cDNA library" /dev stage="adult" 252.-1448
Qy	1294	ACTTAGAAATGTAATGAAATATTCAACAGAACACAGCTGA-----	1345	REFERENCE AUTHORS	Carninci, P., Shibata, Y., Sugahara, N., Hayatsu, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Db	1674	ACTTAGAAATGAAATGAAATGAGTAGTCTTCAAGTTGGTGGCCAGCAGAGGA	1733	TITLE JOURNAL MEDLINE PUBMED	High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253 10349636
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Db	1734	GAGGAAGAGGCCCTGGRTCTGAGCTTCAGTTCAAGCAGCTTGACTCTGT	1793	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AK044474 AK044474 AK044474 AK044474 AK044474 GI:26336516 HTC: CAP trapper. Mus musculus (house mouse) Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
Qy	1398	GATCTAGAGCAAGTCACCTTGCACACTTCTGTGCTTACATTAAATGAGAG	1457	REFERENCE AUTHORS	Carninci, P. and Hayashizaki, Y.
Db	1794	GACCTTAAGTGAATTCAATTAACTGCTTACGTTCACCGCTTGGAAAGGTAGAG	1853	TITLE JOURNAL MEDLINE PUBMED	High-efficiency full-length enriched library, HTC 20-SEP-2003 clone: A930015B13 product: SIMILAR TO SERINE THREONINE KINASE 32 homolog [Homo sapiens], full insert sequence.
Qy	1458	GGTTAT	1463	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AK044474 AK044474 HTC: CAP trapper. Mus musculus (house mouse)
Db	1854	GGATAT	1859	REFERENCE AUTHORS	Carninci, P., Shibata, Y., Sugahara, N., Hayatsu, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
RESULT 2	AK044474	2477 bp mRNA linear HTC 20-SEP-2003		TITLE JOURNAL MEDLINE PUBMED	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
LOCUS		Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone: A930015B13 product: SIMILAR TO SERINE THREONINE KINASE 32 homolog [Homo sapiens], full insert sequence.		2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
DEFINITION		homolog [Homo sapiens], full insert sequence.		2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
ACCESSION	AK044474	AK044474		2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
VERSION		GI:26336516		2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
KEYWORDS		HTC: CAP trapper.		2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
SOURCE		Mus musculus (house mouse)		2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
ORGANISM		Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.		2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
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AUTHORS				2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
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JOURNAL				2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
MEDLINE				2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
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REFERENCE				2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
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MEDLINE				2	Normalizing and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
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GRRPYHRSSTSKEIVNMFEATAIVTPSAWQEMVSLLKKLEPNPNDORFSHLTDI
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QONNNL"

ORIGIN

Query Match 65.2%; Score 968; DB 11; Length 2477;
Best Local Similarity 80.9%; Pred. No. 2.8e-172;
Matches 1218; Conservative 0; Mismatches 245; Indels 43; Gaps 6;

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Qy 121 TACAGAAGAAATGATAACCAAGAAAGATGTGGCAATGAAATAACAAAAGTGGC 180
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Db 790 TAGCTGGCACCAGCCTTACATGGCACCTGAGATGGTCAAGTCCAGTCAAGG 849
Qy 601 ATTCTTTGCTTGTACTGGTGGCTGGAGTGTCACTGGCATATGAACGGCT 660
Db 850 ACTCTTTGCTGACTGGTGGCTGGAGTGTCACTGGCATGGCTGAGGGCC 909
Qy 661 GGAGACCGTATCATATTGCTCCAGTACAGGAATTGTACACACGTTGAGA 720
Db 910 GGAGACCATATCACATCCGGTCACTGGAAATGGTCAAGGAAAGTGTGAGA 969
Qy 721 CGACTGTTGAACCTACCTTACATCCGGTCACTGGAAATGGTCAAGGAAAGT 780
Db 970 CAGCAATTGTAACCTACCTTACATCCGGTCACTGGAAATGGTCAAGGAAAGT 1029
Qy 781 TACTCGAACCTTAATCCAGACCAACGATTTCTGATGCTGGCTGGAGACTTC 840
Db 1030 TGCTGAACCTTAATCCAGACCAACGCTTTCTCAGTGAACATTGAGGATTC 1089

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			Qy 841 ATATGAATGATATAACTGGATGCA GTTTTCAAGAAGGGCTATTCCAGGTTCATTTC 900	
			Db 1090 ACATGAGTGACATGAACTGGACGCCGCTCTGCAGAAGGGCTATTCCAGGTTCATTTC 1149	
			Qy 901 CTAAATAAGGCGAGCTGAATTGATCCTACCTTGAACTTGAGGAAATGATTTGGAGT 960	
			Db 1150 CGACCAAAGGCAGGGCTCAATTGTAACCTGGRAAAATGATTTGGAGT 1209	
			Qy 961 CCAAACCTCTACATAGAAAAGAAAAGGGAGGAGGATATGAGGAAT 1020	
			Db 1210 CCAAACCTCTACAGAAAAGGAAACGACTGGCTAAAGGAGGAAATGAGAAA 1269	
			Qy 1021 GCGATTCTTCAGACATGTTCTGACTCTGTCCAGAAGGGAGTTCA 1080	
			Db 1270 GTGACTCTCTCAGACGTGCCTCTTCAAGAGCATTCTGATGCTGGTCAAGAAAATTTA 1329	
			Qy 1081 TAATTTCAACAGAGAAAAGTAACAGGGACTTAAACAAAGAACAAATCTAGCCT 1140	
			Db 1330 TAATTTCAACAGAGAAAAGTAACAGGGACTTAAACAAAGAACAAATCTAGCCT 1389	
			Qy 1141 TGGAAACAACAAAGAC-----CCACAAAGGTGAGGATGGTCAGAAATAACACTGTAAA 1194	
			Db 1390 TGGAAACAACAAACAAACACAGAGAGGAGGAGGGCCAGAAATAACACCTTAA 1449	
			Qy 1195 GGCCTCATG-----TCTTCTCTCTGGCCAGAAAT-----CTCATGCCAGAAA 1234	
			Db 1450 GTGCTTCAGGCTCTGGGGACAGTGTCTGGCACCTGGCACCTGGGGAA 1509	
			Qy 1235 CTTCTAAATTACATATGTCAGAAAGCTGACAGTAGCTCCCTGCCACTCCACCATG 1293	
			Db 1510 AGTCCTGATTACACACAGAGGCTGACAGGATGACTGAGTCTGGGAGCAGTCTGGCACCTCTG 1569	
			Qy 1294 ACTTAGAAAATGTGAATGAATATATTTCAGAAAAGGAGGACACAGTGA----- 1345	
			Db 1570 ACTTAGAAATATGAATGAGTAGTCTGGGAGCAGTCTGGGAGCAGTCTGGCACCTCTG 1629	
			Qy 1346 -----AGGGTCTGGCCCTGAGCTCTTGGAAAGTCAATTCAACTGTGT 1397	
			Db 1630 GAGGAAGAGGCCCTGGCTCTGAGCTCTTCAGTCCAGGCTGACTCTGT 1689	
			Qy 1398 GATCTAGAGCAAGTCACTTAGGCACTTTCTGTGCTTACATTATGCTAAATGAGAG 1457	
			Db 1690 GACCTTAAGTGAATCATTTAACCTGCTCCCTGTTAGTTCACCGCTTGGAAAGGTAGAG 1749	
			Qy 1458 GTTTAT 1463	
			Db 1750 GGATAT 1755	
		RESULT 3	AK036266	
		LOCUS	AK036266	3766 bp mRNA linear HTC 19-SEP-2003
		DEFINITION	AK036266	16 days neonate cerebellum CDNA, RIKEN full-length enriched library, clone:9630050F05 product:SIMILAR TO SERINE THRONTINE KINASE 32 homolog [Homo sapiens], full insert sequence.
		ORGANISM	AK036266	Mus musculus (house mouse)
		KEYWORDS	AK036266.1 GI:26331271	HTC, CAP trapper.
		SOURCE	AK036266	Mus musculus (house mouse)
		ORGANISM	AK036266	Eukaryota; Metazoa; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
		REFERENCE	1	Carninci, P. and Hayashizaki, Y.
		AUTHORS	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
		TITLE	3	High-efficiency full-length cDNA cloning
		JOURNAL	4	Meth. Enzymol. 303, 19-44 (1999)
		MEDLINE	5	99279253
		PUBMED	6	10349636
		REFERENCE	2	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
		AUTHORS	3	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
		TITLE	4	Normalizing and subtracting cDNA libraries for rapid discovery of new genes

JOURNAL	Genome Res.	10 (10), 1617-1630 (2000)
MEDLINE	20499374	
PUBMED	11042159	
REFERENCE		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuwra, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	
JOURNAL	Genome Res.	
MEDLINE	20530913	
PUBMED	11076861	
REFERENCE		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	
TITLE	Functional annotation of a full-length mouse cDNA collection	
JOURNAL	Nature	
REFERENCE	409, 685-690 (2001)	
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
JOURNAL	Nature	
REFERENCE	420, 563-573 (2002)	
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imottani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Yokohama, Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
	Please visit our web site for further details.	
	URL: http://genome.gsc.riken.go.jp/	
	URL: http://fantom.gsc.riken.go.jp/	
FEATURES	source	
	1. .3766 /organism="MUS musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:9630050F05" /db_xref="MGI:2400675" /db_xref="taxon:10090" /clone="9630050F05" /tissue_type="cerebellum" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="16 days neonate"	
CDS	243..1439	
	/note="unnamed protein product; SIMILAR TO SERINE THREONINE KINASE 32 homolog [Homo sapiens] (SPTR AAH21666, evidence: FASTY, 95.5%ID, 94.5%length, match=471) putative"	

QY	841	ATATGATGATAAACTGGATGAGTTTCAGAAGGGCTCATCCAGGTTCAATTCCAGGTTTCATTTC 900	found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
DB	1081	ACATGAGTGCATGAACTGGGACCTCCTGGAGGGCTCATTCAGGTTTCATTTC 1140	Plate: LLAM10041 row: h column: 24 High quality sequence stop: 764.
QY	901	CTAATTAAGGGGGCTGAATTGTGACTTACCTTGAACTTGAAGGAATGTTGAGT 960	Location/Qualifiers
DB	1141	CGACCAAAGGGGGCTCAATTGTGACCCCACTTGTAACTGGAGAAATGTTGAGT 1200	1. .893 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4375751" /tissue_type="hippocampus" /lab_host="DH10B"
QY	961	CCAAAACCTCTACATAAGAAAAAAAGCGTCTGGCAAAGGAGGATATGAGGAAT 1020	
DB	1201	CCAAAACCTCTACAAAGAAAAAGAACGACTGGCTTAAAGGGAGAAATGAAGAAA 1260	
QY	1021	GGGATTCCTCTCTAGACATGCTTCTTCAAGGCCCTTGACTCTGTCCAGAAGGTTCA 1080	/note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XbaI (gtcgag); Oligo-dR primed using primer 5'-TTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
DB	1261	GTGACTCCCTCTAGACGTGGCTTCAAGGGATCTGTGATGCTGGTTCAGAAAGAATTAA 1320	
QY	1081	TAATTTCACAGAGAAAGTAAACAGGGACTTAACAAAGACAACCAATCTAGCCT 1140	
DB	1321	TAATTTCACAGAGAAAGTAAACAGGGACTTAATCAGAGACAAGGAATCTAGCCT 1380	
QY	1141	TGGAAACAACCAAGAC-----CCACAAAGGTGAGGATGGTCAGAATAACACTTGAAA 1194	
DB	1381	TGGAAACAACCAACACAGAGAAAGTAAACAGAGACAACAGATAACACCTATAAA 1440	
QY	1195	GGCCTCATG-----TCTCTCTCTGGGACAAT-----CTCATGCCAGAAA 1234	ORIGIN
DB	1441	GTGCTTCGGAGTCTTCGGGGACAGTGTCTGGGACAGTCTGGCACCTGGCGGGAA 1500	Query Match Score 710.6; DB 10; Length 893; Best Local Similarity 97.3%; Pred. No. 1e-123; Matches 733; Conservative 0; Mismatches 19; Indels 1; Gaps 1;
QY	1235	CTTCTTAATTACATAATATGTCAAGAAAAGCTGACAGTAGCTCCTGCCACT-CACACACCATG 1293	QY 230 GGGCTGAGGACCCCTTCTGGTTAATTGTGGTATTCCTCCAAAGATGAGGAAGACAT 289 6 GGGCTGAGGACCCCTTCTGGTTAATTGTGGTATTCCTCCAAAGATGAGGAAGACAT 65
DB	1501	AGTCCTGATTATCACACACAGAAAGCTGACAGGTGTCCTGCCACTCTGCACACTCATG 1560	Db 290 GTTCATGTTGGGGACCTCTGGTGGGACCTGGGTATACACTTGCAACAGAACGT 349 66 GTTCATGTTGGGGACCTCTGGTGGGACCTCTGGTGGGACACTGGGTATACACTTGCAACAGAACGT 125
QY	1294	ACTTAGAAAATGTGAATATATTTCAAAAAAGGGAGCCACAACAGTGA----- 1345	QY 350 CCACTTCAGGAAGAAACAGTGAAAGCTCTCATCTGGTGGGCTCATGGCCCTGGACTA 409 126 CCACTTCAGGAAGAAACAGTGAAAGCTCTCATCTGGTGGGCTCATGGCCCTGGACTA 185
DB	1561	ACTTAGAAATATGAATGAGTAGTGTCTCGAAGTGGTGGCAGGACTCTGCAGGGACAGGA 1620	Db 410 CCTGAGAACCCGGCATCATTCAACAGGATATGAGGCTGACAATATTTACTTGACGA 469 186 CCTGAGAACCCGGCATCATTCAACAGGATATGAGGCTGACAATATTTACTTGACGA 245
QY	1346	-----AGGGTCTGGGGCTGAGCTCCTGGAAAGGTCAATTCA-CATCAATCAACTGTGT 1397	QY 470 ACATGGGCACGTGCACATCACAGATTCAACATTGGTGGCATGCTGCCAGGGACACA 529 246 ACATGGGCACGTGCACATCACAGATTCAACATTGGTGGCATGCTGCCAGGGACACA 305
DB	1621	GAGGAAGAGGGCCCTGGTCTGAGCTTCAAGTCCAGCTCAGGACGATTGACTCTGT 1680	Db 530 GATTACCCATGGCTGGCACCAAGGCTTACATGGGACCTGTGTTCAAGCTCCAGAAA 589 306 GATTACCCATGGCTGGCACCAAGCCTTACATGGGACCTGTGAGTGTCAAGTCCAGAAA 365
QY	1398	GATCTAGAGCAAGTCACCTAGCCACTTCTGTGCTTTACTTTATTCAATGAGAG 1457	QY 590 AGGAGCAGGGCTATTCTCTGGTGTGACTGGTCCCTGGGAGTGACGGCATATGAACT 649 366 AGGAGCAGGGCTATTCTCTGGTGTGACTGGTCCCTGGGAGTGACGGCATATGAACT 425
DB	1681	GACCTTAAGTGAATCATTTAACTGCTTCCCTGTGTTAGTTACCGCTTGGAAAGTAGAG 1740	Db 650 GCTGAGAGGGGGAGACCGTATCATATTGCTCCAGTACTTCCAGGAAGGAATTGTACA 709 426 GCTGAGAGGGGGAGACCGTATCATATTGCTCCAGTACTTCCAGGAAGGAATTGTACA 485
QY	1458	GGTTAT 1463	Db 709 CACGTTGAGGAGCTGTGTRACTACCTTCTGCTGGTCAACAGGAATATGGTGTCACT 769 486 CACGTTGAGGAGCTGTGTRACTACCTTCTGCTGGTCAACAGGAATATGGTGTCACT 545
DB	1741	GGATAT 1746	COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
RESULT	4		
LOCUS	BG036777	893 bp mRNA Homo sapiens CDNA clone IMAGE:4375751 5', linear EST 24-JAN-2001	
DEFINITION	602286992F1	mRNA Sequence.	
ACCESSION	BG036777		
VERSION	BG036777.1	EST. GI:12432521	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 893)		
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/.		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be		

Qy	890 AGGTTCATTCATAAAAGGCCAGGCTGAATTGTGATCCTTGAACCTTGAGGAAT	949	TITLE JOURNAL	Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)			
Db	666 ACGTTTCATTCCATTAAAGGGCTGAATTGTGATCCTTGAACCTTGAGGAAT	725	COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.			
Qy	950 GATTGGAGTCCAAACCTCTACATAAGAAAAA	982	FEATURES SOURCE	AK082468 Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230053G02 product:serine threonine kinase 32, full insert sequence.			
Db	726 GA-TTGGGTCCAAACCTTACATAGAAAAA	757	LOCATION ORGANISM	AK082468 GI:26349720 HTC; CAP trapper. Mus musculus (house mouse) Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	Carninci, P. and Hayashizaki, Y.	1	CDS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. High-efficiency Full-length cDNA cloning. Meth. Enzymol. 303, 19-44 (1999)			
AUTHORS	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	2	FEATURES DEFINITION	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	3	COMMENT	1049636			
PUBMED	11042159	4	FEATURES DEFINITION	Carninci, P., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishime, T., Harada, A., Yamamoto, R., Matsutomo, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)			
AUTHORS	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	5	COMMENT	20530913			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)	6	FEATURES DEFINITION	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection. Nature 409, 685-690 (2000)			
PUBMED	11076861	7	COMMENT	4			
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection. Nature 409, 685-690 (2000)	8	COMMENT	3			
AUTHORS	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	9	COMMENT	2			
JOURNAL	Nature 420, 563-573 (2002)	10	FEATURES DEFINITION	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	11	COMMENT	1
PUBMED	12309441	12	FEATURES DEFINITION	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection. Nature 409, 685-690 (2000)	13	COMMENT	1
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection. Nature 409, 685-690 (2000)	14	FEATURES DEFINITION	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	15	COMMENT	1
AUTHORS	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	16	COMMENT	1			
JOURNAL	Nature 420, 563-573 (2002)	17	FEATURES DEFINITION	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	18	COMMENT	1
PUBMED	12309441	19	FEATURES DEFINITION	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection. Nature 409, 685-690 (2000)	20	COMMENT	1
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection. Nature 409, 685-690 (2000)	21	FEATURES DEFINITION	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	22	COMMENT	1
AUTHORS	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	23	COMMENT	1			
JOURNAL	Nature 420, 563-573 (2002)	24	FEATURES DEFINITION	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	25	COMMENT	1
PUBMED	12309441	26	FEATURES DEFINITION	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection. Nature 409, 685-690 (2000)	27	COMMENT	1
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection. Nature 409, 685-690 (2000)	28	FEATURES DEFINITION	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	29	COMMENT	1
AUTHORS	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	30	COMMENT	1			
JOURNAL	Nature 420, 563-573 (2002)	31	FEATURES DEFINITION	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	32	COMMENT	1
PUBMED	12309441	33	FEATURES DEFINITION	The RIKEN Genome Exploration Research Group Phase II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature 420, 563-573 (2002)	34	COMMENT	1
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature 420, 563-573 (2002)	35	FEATURES DEFINITION	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	36	COMMENT	1
AUTHORS	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahirra, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyoda, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	37	COMMENT	1			
JOURNAL	Nature 420, 563-573 (2002)	38	FEATURES DEFIN				

Qy	303	GACCTCTGGAGACCTGCAACAGAACGTCCACTTCAAGGAA	362		TITLE	Adams, M.D. and Cargill, M.
Db	669	GACCTGCTGGTGGGACCTGCGCTTACCACTACGGAAATGTGCAAGAG	728		JOURNAL	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
Qy	363	GAACAGTGAAGCTCTTCATCTGTGAGCTGGACTACCTGGAGAACCCAG	422		PUBLISHED	Science 302 (5652), 1960-1963 (2003)
Db	729	GGGACCGTGAAGCTGTACATCTGTGAGCTGGCTGGAGTACCTGCAGGTAC	788		REFERENCE	(bases 1 to 1245)
Qy	423	CCCATCATTCAACAGGGATATGAAAGCATAATTCTTACTTGACAAACATGGGCAACGTG	482		AUTHORS	Clark, A.G., Golanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Db	789	CACATCATCCACAGAGATCAAGCCAGAACATCCTACTGGATGAGCATGGCAACGTG	848		TITLE	Direct Submission
Qy	483	CACATCACAGATTCAACATTGCTGGCATGGCAACAGATTACCATG	542		JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Db	849	CACATAACGGACTTCAACATGCCAACGGTCTCTGAAGGAGTGAAGGCTCCTCGTG	908		COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
Qy	543	GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAAGTCAGCTCCAGAAAAGGAGCAGGC---	599		FEATURES	Location/Qualifiers
Db	909	GCTGGCACGAAGCCCTACATGGCCCCTGAAGTGTGAGGGCCT	968		Source	1. 1245 /organism="Mus musculus" /mol type="genomic DNA" /db_xref="taxon:10090" <1..>1245 /locus_tag="HCM2506"
Qy	600	--TATTCTCTTGTGTTGACTGGTGCCTGGAGTGAAGTGTGAGA	656		ORIGIN	
Db	969	GGGTACTCATACCCCGTGGACTGGTCACTGGCTGACTGGCTGTCAGCCTGACAGCTGTCAGCGTGAAG	1028			
Qy	657	GGCGGAGACCCATTACATTTCGCTCCAGTCAAGGAATTGTACACAGTT	716		Query Match	37.3%; Score 553.6; DB 29; Length 1245;
Db	1029	GGCTGGAGCCATTATGAGATCCACTCAAGCCACACCTCAACATGTTTC	1088		Best Local Similarity	69.8%; Pred. No. 3.1e-94;
Qy	717	GAGAGACTGTGTAACCTACCCATTCTGCTGGTCAAGTCTCTAAA	776		Matches	780; Conservative 0; Mismatches 329; Indels 9; Gaps 2;
Db	1089	AAGGTGGAGCGTGTCCACTACTCCTCAACGGGATGGTGTGACGGCATG	1148		Qy	3 ATGGGACCGAACACTTCAGAAACACCAGTGTGATGAAGATGTCAACTTT
Qy	777	AAGCTACTGAACTTAATCCAGACCAAGCATTCTCAGTTATCTGATGTCCAGAACCTTC	836		Db	1 ATGGGGGGAAACCTCCACAGCCCCACTCCACAGCCCAGTGTGCAACTTT
Db	1149	AAGCTGCTGACCAAGGACCTCTGAGCCGCTTGTCAAGTCCTGTGACATCCAGGATG	1208		Qy	63 GACCACTTGAATTTCGAGCCATTGGAAAGGCAAGTTGGGAGGGCTGCATTGTA
Qy	837	CCGTATATGATAATGATAAACTGGATGAGCTTTCAGAAAGGGCTCATTCAGGTT	896		Db	61 GACCACTTCCAGATCCTGCGGCCATTGGAAAGGAAAGTTGGATGCTGCATGTTG
Db	1209	ACCTACCTGGCTGACATGAACACTGGGATATTGAGAAGGGCCCTGATGCTGGTT	1268		Qy	123 CAGAAGATGATAACCAAGAAGATGTCGGAATGAGTACATGATAACAAAGTGGTG
Qy	897	ATTCTAAATAAGGCAAGGTGAATTGTGATGCTCCTAACCTTGAACATTGATTG	956		Db	121 CAGAAGGGAGACACAAGAAGATGTGATGCTGAGTACATGAAAGGAAAGTGTG
Db	1269	GTGCCCAATAAGGGAGACTGAACTGTGACCCACATTGAAAGAAATGATGCTA	1328		Qy	183 GAGGGCAATGAAAGTGGAAATGTTCTCAAGGAACCTCAGATCAGGGTCTGGAGCAC
Qy	957	GAGTCCAACCTCTACATAAGAAAAAGGTCTGGCAAAG---AAGGAGAAGGATATG	1013		Db	181 GAGAGGGATGAGGTGGGAAACCTGTTCCGGGAGCTGGCAGTATGAGGAC
Db	1329	GAATCCAAGCCACTTCACAAAAGGAGAGGTGGCTCAGAGAACAGC	1388		Qy	243 CCTTCCCTGGTAATTGGTGTATTCCCTCAAGATGTTCATGGTGGT
Qy	1014	AGGAAATGGGATTCCTCTAGACATGTCTTCAAGGACCCATTGACTCTGTCCAGAAAG	1073		Db	241 CCCTTCCCTGGTAACCTATGGTACTCCTCCAGGTGAGGAAGACATGTTCATGGTGGT
Db	1389	ACAAAGGACAGCTTCACATTCAACCGAGAGAACACTCAGGGCA	1486		Qy	303 GACCTCCCTGGGGAGACCTGGTTATCACCTGCAAACAGAACGTCCACCTTCAGGAA
Qy	1074	GAGTCTCATAAATTTCACAGACATGTCTTCAAGGACCCATTGACTCTGTCCAGGAAAG	1111		Db	241 GACCTCCCTGGGGAGACCTGGTTATCACCTGCAAACAGAACGTCCACCTTCAGGAG
Db	1449	GAGTCTCATATTCAACCGAGAGAACACTCAGGGCA	1486		Qy	363 GAAACAGTGAAGCTTCACTGAGCTGGGAGCTACCTGAGAACACCAG
RESULT	6				Db	301 GACCTCCCTGGGGAGACCTGGTTATCACCTGCAAACAGAACGTCCACCTTCAGGAG
AY406286					Qy	363 GAAACAGTGAAGCTTCACTGAGCTGGGAGCTACCTGAGAACACCAG
LOCUS	AY406286	1245 bp	DNA	linear	Db	361 GGGCCCTGAGGCTACATCTGGGAGCTGGATGCTGAGCATGGGAC
DEFINITION	Mus musculus HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence,				Qy	423 CGCATCTTCAAGGGATATGAAAGCTTACATTTCAGGAACTGGGACCGTG
ACCESSION	AY406286				Db	483 CACATCAGATTCAACATGGCCTGCGATGCTGGCTGGGGAGTGAAGCTGGT
VERSION	AY406286.1				Qy	483 CACATCAGATTCAACATGGCCTGCGATGCTGGCTGGGGAGTGAAGCTGGT
KEYWORDS	GSS.				Db	481 CACATAACGGACTTCAACATGGCCTGCGATGCTGGCTGGGGAGTGAAGCTGGT
SOURCE	Mus musculus (house mouse)				Qy	541 GCTGGACGAAAGCCTACATGGCCCTGAGGCTGAGCATGGGAC
ORGANISM	Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				Qy	600 ---TATTCTCTGGTGTGTTGACTGGCTGGCTGGGGAGTGAAGCTGGT
REFERENCE	1 (bases 1 to 1245)				Db	601 GGTAATCTCATACCCGGTGGACTGGTCACTGGGTCTGAGCTGTCGA
AUTHORS	Clark, A.G., Golanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,				Qy	660 660
						657 GGGGGAGACCGTATCATATTGGCTCCACATTCAGGAAATTGTCACACGGTT

Best Local Similarity		Pred. No. 7.9e-92;	
Matches	Conservative	0;	Mismatches
661 GGCTGGGCCATATGAGATCCACTCAGGCCACCCATTGTGAGATTCTCAACATGTTTC	720	Qy	3 ATGGAGCCAAACCTTCAAGAAAACCACCGTTCAGGGTCAAGGAAATTGGTCAACTTCTT
717 GAGACGACTGTAACTTACCTTACGGTGGTGGTCAGGGAAATTGGTCAACTTCTTAAA	776	Qy	62
721 AAGGTGGAGCGTCCACTCTCCACGTTGGTGGGGATGGTCAAGTGGCATGAG	780	Db	1 ATGGGGAAACCACTCCCACAGCCCCCTGAGGGAGTGGTCAAGTGGCATGAG
777 AAGCTACTCGAACCTAACTCCAGACCCAAACGATTTCTCAGGAAATGGGAAACTTC	836	Qy	60
781 AAGCTGCTGACATGAACTGGGATGGCAGTGGTCAAGTCTTGAAAGGTGGCTGAG	840	Db	61 GACCATTTCAGATCTGGGCCATTGGTAAAGGTATGCAAGTGGCATGAG
837 CCGTATATGATAATGATAAACTGGGATGGCAGTTCTCAGGAAATGGGAAACTTC	896	Qy	63 GACCACTTGTGAAATTGGGAGCCATTGGGAGGTCTGGGAGGTGGCTGATGGTCA
841 ACCTACCTGGTGAACATGAACTGGGATGGCAGTGGTCAAGTCCAGAGCATG	900	Db	122 GAGAAGGAGAACACTAAGAAATGTAATGCAAGTGGCATGAAACAGGAAATGG
897 ATTCTTAATAAGGCAGGGCTGAAATTGTGATCCTGAGGGAAATGATTTTG	956	Qy	123 CAGAAGGAGTACACAGGAAATGGGAGTACATGAGTACATGGGAGGTGGCTG
901 GTGCCAATAAAGGGAGACTGAACCTGAGGGAGACTGTGAACTGGGAGCTGAG	960	Db	121 GAGAAGGAGAACACTAAGAAATGTAATGCAAGTGGCATGAAACAGGAAATGG
957 GAGTCCAAACCTCTACATAAGAAAAAGGGTCTGGCAAGGAACTTGGCTGAG	1013	Qy	123 CAGAAGGAGTACACAGGAAATGGGAGTACATGAGTACATGGGAGGTGGCTG
961 GAATCCAAGGCAACTCACAAAGGAAGAAGGAGGAGCTGGCACTTCAAGAGCAGC	1020	Db	182 GAGAGGGAGTAGGTTGGGAATGTTTCGGGAGCTGGCATGAACTGGCATGAG
1014 AGGAATATGGGATTCTTACATTAAGAAAGGGTCTGGCAAG - - - AGGAGAAGGATATG	1073	Qy	183 GAGGGGAGTAGGTTGGTACTCCCTGGTCAATTGGTCAAGTGGCATGAG
1021 ACAAGGACAGGCTGTCCCTGAATGGACACACTGGAGAACACTGGAGGGCA	1080	Db	181 GAGAGGGAGTAGGTTGGGAGCTGGCACTTCAAGGAGCATGGTCAAGAGCAGC
1074 GAGTTCAATAATTTCACAGACATGTCCTTCAGAGGACCTTGACTCTGTCAG	1111	Qy	242 CCTTCCTGGTTAAATTGGGAGCCTGGCTTACCTTCAAGGAACTTCAGGAA
1081 GAGTTCATCATATTCAACCGAGAACACTGGAGAACACTGGAGGGCA	1118	Db	243 GACCTCCTGGTTAAATTGGGAGCCTGGCTTACCTTCAAGGAACTTCAGGAA
RESULT 7			
LOCUS	AY406284	1245 bp	DNA linear
DEFINITION	Homo sapiens HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence,		GSS 12-DEC-2003
ORGANISM	Homo sapiens		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
REFERENCE	AY406284		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VERSION	AY406284.1		1 (bases 1 to 1245)
KEYWORDS	GI:39762258		Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
SOURCE	GSS.		Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
ORGANISM	Homo sapiens (human)		Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
REFERENCE	AY406284		Adams,M.D. and Cargill,M.
AUTHORS			661 Inferring nonneutral evolution from human-chimp-mouse orthologous
TITLE			gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)		717 GAGACGACTGTGTAACTTACCCCTGGTCACTTCAA
PUBMED	14671302		776
REFERENCE	2 (bases 1 to 1245)		721 AAGGTGGAGCTTCACTACTCCTCCAGTGGCAAGGGATGGCTGAGGG
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,		777 AAGCTACTCGAACCTAATCCAGACCAACGATTTCAGTGTCCAGAACTTC
	Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,		836 Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
	Adams,M.D. and Cargill,M.		840 Adams,M.D. and Cargill,M.
TITLE			781 Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,		837 CGGTATATGAAATGATAAACTGGGATGGCTCAATTCCAGGTTCATT
COMMENT	Rockville, MD 20850, USA		896 GAGTCCAAACCTCTACATAAGAAAAAGGGTCTGGCAAGAGAAATGATT
FEATURES	This sequence was made by sequencing genomic exons and ordering		956 /db_xref="taxon:9606"
source	them based on alignment.		901 GTGCCCAATAAGGGCGCACTGACTGGGACGGGACTCTGAGGGATGATT
gene	Location/Qualifiers		960 /locus_tag="HCM2506"
ORIGIN	1. .1245 /organism="Homo sapiens"		961 GAATCCAAGCCACTCACAAAGAACGATCCAGGGATGGC
	/mol_type="genomic DNA"		1020 1014 AGGAATATGGGATTCTCTCAGACATGTCCTTCAGAACCTTGACTCTGTCAGAAG
Query Match	36.4%: Score 540.8; DB 29; Length 1245;		1073

1021	ACAAAGGACAGCTGCCCGCTGAATGGACACCTGGCAACTGTGGACTTACCATCTGGCTACGGAG 360	Db
1074	GAGTTCAATAATTTCACAAGAAAAAGTAAACAGGGAA 1111	Qy
1081	GAATTCAACAGAGAACGCTCAGGGCA 1118	Db
RESULT 8		
LOCUS	AY406285	DNA
DEFINITION	Pan troglodytes HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	GSS 12-DEC-2003
VERSION	AY406285.1	GI:39762259
KEYWORDS	Pan troglodytes (chimpanzee) Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	
REFERENCE	1 (bases 1 to 1245)	
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios	
JOURNAL	Science 302 (5652), 1960-1963 (2003)	
PUBMED	14671302	
REFERENCE	2 (bases 1 to 1245)	
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	
JOURNAL	Direct Submission	
COMMENT	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
FEATURES	This sequence was made by sequencing genomic exons and ordering them based on alignment.	
Source	Location/Qualifiers	
	1..1245 /organism="Pan troglodytes"	
	/mol type="genomic DNA"	
	/db_xref="taxon:9598"	
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Qy	3 ATGGGAGCCGAACACTTCAGAAAACCACCAAGTGTGTTGATGAAATGAAAGATGTCAACTT 62	
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REFERENCE	Carninci,P. and Hayashizaki,Y.	
AUTHORS	1 Carninci,P. and Hayashizaki,Y.	
JOURNAL	High-efficiency full-length cDNA cloning	
MEDLINE	1 Meth. Enzymol. 303, 19-44 (1999)	
1	99279253	

PUBMED	10349636	REFERENCE	
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	AUTHORS	
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	TITLE	
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	JOURNAL	
MEDLINE	20499374	MEDLINE	
PUBMED	11042159	PUBMED	
REFERENCE		REFERENCE	
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuurra, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	AUTHORS	
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	TITLE	
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)	JOURNAL	
MEDLINE	20530913	MEDLINE	
PUBMED	11076861	PUBMED	
REFERENCE		REFERENCE	
AUTHORS	The RIKEN Genome Exploration Research Group Phase II team and the FANTOM Consortium.	AUTHORS	
TITLE	Functional annotation of a full-length mouse cDNA collection	TITLE	
JOURNAL	Nature 409, 685-690 (2001)	JOURNAL	
REFERENCE		REFERENCE	
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	AUTHORS	
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	TITLE	
JOURNAL	Nature 420, 563-573 (2002)	JOURNAL	
REFERENCE	6 (bases 1 to 2161)	REFERENCE	
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	AUTHORS	
TITLE	Direct Submission	TITLE	
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	JOURNAL	
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	COMMENT	
FEATURES	Please visit our web site for further details.	FEATURES	
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	URL: http://fantom.gsc.riken.go.jp/		
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ORIGIN

	Query	Match	Score	Length
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Qy	150	GCAATGAAAGTACATGAAATAACAAAAGTGGCTGGAGCGCAATGAAAGTGGAGAAATGTCTTC	209	
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Qy	210	AGGAACCTCCAGATCATGGGGCTCTGGAGCACCCTTCTGGTTAATTGTGGTATTCC	269	
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Qy	270	TTCCAAGATGAGGAAGACATGTTCATGGTGGCTGGACCTCCTGGCTGGGTGAGACCTGGCT	329	
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Qy	330	TATCACCTGCAACAGAACGTCACATTCAAGGAAGAACAGTGAAGGCTCTCATCTGTGAG	389	
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Qy	390	CTGGTCAATGCCCTGGGACTACCTGAGAACCCAGGCATCATCAGGATATGAAGGCCT	449	
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Qy	450	GACAATATTTCAGTGGCACATGGGCACATCACAGATTCAACATTCGCTGGCG	509	
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Db	890	GAGATCTTCCACTCTTGTCAATGGGGACTGGCTACTGGGACTACGAGGATGGCTACGAGGATGGCTCA	949	
Qy	624	TCCTGGGAGTGA CGGCATATGAAACTGCTGAGAGGCCGTTATCATATTGCTCC	683	
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Qy	684	AGTACTTCCAGGAAATTGTTGAGACGACTGTTGACTGTGTAACTTACCCCTCT	743	
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Best Local Similarity 98.9%; Pred. No. 1.1e-77; Matches 469; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy	804	CGATTTCTCAGTTATCTGATGTCCAGAACACTTCCCGTATATGAAATGAACTGGGAT	863
Db	1130	CGGTCTCCAGTCTCCAGTCTCCAAGACATGCGAGACGCCCATCGCTGGCCAC	1189
Qy	864	GCAGGTTTCAGAAGAGGGCTCATTCCAGGTTTCATTCTAAATAAGGCAGGCTGAAATTGT	923
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Qy	1044	-----CTTCAGAGGACCTTGAACTCTGTCAGAGGAGTTCATAAATTCAACAGAGAA	1097
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RESULT 10
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DEFINITION AGENCOURT_7970922 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6163821
ACCESSION BU156055
VERSION BU156055.1 GI:22669587
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 829)
AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cagsr@mail.nih.gov
Tissue Procurement Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 465.

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Average insert size 2 kb. Library constructed by Life
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VERSION BU412592.1 GI:25905263
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ORGANISM Gallus gallus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
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Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 836)
AUTHORS Boardman,P.E., Sanz-Bzquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Pong,W.T., Tickle,C., Brown,W.R.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 2235534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
Email: Simon.Hubbard@umist.ac.uk.
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ORIGIN

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ACCESSION	BG033516	mRNA sequence.	

VERSION BG033516.1 GI:12425892

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 869)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Straussberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DRP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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Location/Qualifiers

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ORIGIN

Query Match	Score 426.8;	DB 10;	Length 869;
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Qy	420 CAGGGCATTCATTCAACGGGATATGAAGCCTGACAATATTCTACTGAGAACATGGGC	477	
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 site_2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with Oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into PYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CGAACTGAAT. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

	Query Match	Score	DB	Length
Qy	28.1%; Score 417.8;	14;	DB 1;	Length 724;
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Db	1160 ACAAGGTGAGGGATGGTCAAGATAACAACTTGTAAAGGCCCTCATG-----TC 1205			
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FEATURES

	source
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Location/Qualifiers	1..711
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/lab_host:	"DH10B (T1 phage resistant)"
/clone_lib:	"NIH_BMAP_FW0"
/note:	"Organ: Brain; Vector: PYX- Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Dr. M. Bento Soares, University of Iowa, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
ORIGIN	
Query Match	26.2%;
Best Local Similarity	Score 388.8;
Matches	Pred. No. 3.7e-63;
Qy	Mismatches 187;
Db	Indels 6;
Qy	Gaps 1;

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Search completed: June 26, 2004, 23:07:47
 Job time : 2836 sec^s

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 22:20:22 ; Search time 500 Seconds

(without alignments)
 13605.835 Million cell updates/secTitle: US-10-667-442-1
 Perfect score: 1485
 Sequence: 1 ccatggaaacacttca.....taaaaaaaaaaaaaa 1485Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1485	100.0	1485	13 US-10-667-442-1	Sequence 1, Appli
3	1485	100.0	1485	15 US-10-254-869-1	Sequence 1, Appli
4	1228.6	82.7	1281	16 US-10-410-764-100	Sequence 100, App
5	1188.2	80.0	1594	13 US-10-362-892-44	Sequence 44, Appli
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7	1188.2	80.0	1594	16 US-10-288-798-44	Sequence 44, Appli
8	1186.2	79.9	1191	9 US-09-841-683-10	Sequence 10, App
9	1184.6	79.8	1191	16 US-10-410-764-102	Sequence 102, App
10	1162.6	78.3	1675	9 US-09-841-683-12	Sequence 12, Appli
11	1160.6	78.2	1224	9 US-09-841-683-8	Sequence 8, Appli
12	1029.4	69.3	2063	16 US-10-108-260A-231	Sequence 231, App
13	672.8	45.3	678	13 US-10-276-774-239	Sequence 239, App
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ALIGNMENTS

RESULT 1
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 ; Sequence 1, Application US/09801876B
 ; Patent No. US20020127683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YB, Jane et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEAR ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
 ; FILE REFERENCE: CL001160
 ; CURRENT APPLICATION NUMBER: US/09/801,876B
 ; CURRENT FILING DATE: 2001-03-09
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1485
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-801-876B-1

Query Match 100.0%; Score 1485; DB 9; Length 1485;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1485; Conservative 0; Description

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 ; Sequence 1, Application US/10667442
 ; Publication No. US20040043466A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL001160DIV II
 ; CURRENT APPLICATION NUMBER: US/10/667,442
 ; CURRENT FILING DATE: 2003-09-23
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1485
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ;
 US-10-667-442-1

Query Match 100.0%; Score 1485; DB 13; Length 1485;
 Best Local Similarity 100.0%; Pred. No. 0;
 Mismatches 0; Indels 0; Gaps 0;
 Matches 1485; Conservative 0;

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 Db 1 CCATGGGAGCGAACACITCAAGAAAAACCCAGTGTGTTGATGAAAAATGAGATGTCAACT 60
 Qy 61 TTGACCACTTTGAAATTGGAGCCATTGGGAAAGGGCAGTTTGGGGAGGGCTCTGCATTTG 120
 Db 61 TTGACCACTTTGAAATTGGAGCCATTGGGAAAGGGCAGTTTGGGGAGGGCTCTGCATTTG 120
 Qy 121 TACAGAAGAAATGATAACCAAGAAGATGTGCAATGAAATAAACAAAGTGG 180
 Db 121 TACAGAAGAAATGATAACCAAGAAGATGTGCAATGAAATAAACAAAGTGG 180
 Qy 181 TGGAGGCCAATGAGTGAGAAATGGCTTCAAGGAACCTCCAGATCATGGGAGG 240
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
 CURRENT APPLICATION NUMBER: US/10/254,869
 CURRENT FILING DATE: 2002-09-26
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 1485
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 ORGANISM: Human
 US-10-254-869-1

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541	TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTCACTCCAGAAAGGAGGGCT	600	100.0%	1485	100.0%	0	0	0	0	0	
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601	ATTCTTGTGACTGGTCCAGTACTCCAGAACATTGTACACACAGTTGAGA	720	100.0%	1485	100.0%	0	0	0	0	0	
661	GGAGACCGTATCATATCGTCCAGTACTCCAGAACATTGTACACACAGTTGAGA	720	100.0%	1485	100.0%	0	0	0	0	0	
661	GGAGACCGTATCATATCGTCCAGTACTCCAGAACATTGTACACACAGTTGAGA	720	100.0%	1485	100.0%	0	0	0	0	0	
721	CGACTGTGTAACTTACCCCTCTGGCTGGATGCTCACTCTAAAGAAC	780	100.0%	1485	100.0%	0	0	0	0	0	
721	CGACTGTGTAACCTACCTGGCTGGATGCTCACTCTAAAGAAC	780	100.0%	1485	100.0%	0	0	0	0	0	
781	TACTCGAACCTAATCCAGAACAACTTACCTGGCTGGATGCTCACTCTAAAGAAC	840	100.0%	1485	100.0%	0	0	0	0	0	
781	TACTCGAACCTAATCCAGAACAACTTACCTGGCTGGATGCTCACTCTAAAGAAC	840	100.0%	1485	100.0%	0	0	0	0	0	
841	ATATGAATGATAATAACTGGGATGGCAGTTTCAGAACAGGCTCATTCCAGGTTTCATTTC	900	100.0%	1485	100.0%	0	0	0	0	0	
841	ATATGAATGATAATAACTGGGATGGCAGTTTCAGAACAGGCTCATTCCAGGTTTCATTTC	900	100.0%	1485	100.0%	0	0	0	0	0	
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901	CTATAAAGGCAGGCTGAATTGTGATCCTACCTTGAAACTGATTGGAGT	960	100.0%	1485	100.0%	0	0	0	0	0	
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961	CCAACCTCTACATAAGAAAAAGGCTTGGCAAAGAACAGGATAATGAGGAAT	1020	100.0%	1485	100.0%	0	0	0	0	0	
1021	GCGATTCTTCAGACATGTCTCAAGAGGCACCTTGACTCTGTCCAGAACGGAGTTCA	1080	100.0%	1485	100.0%	0	0	0	0	0	
1021	GCGATTCTTCAGACATGTCTCAAGAGGCACCTTGACTCTGTCCAGAACGGAGTTCA	1080	100.0%	1485	100.0%	0	0	0	0	0	
1081	TAATTTCAACAGAGAAAAGTAAACAAAGGACTTAACAAAAGAACAAACTTAGCCT	1140	100.0%	1485	100.0%	0	0	0	0	0	
1081	TAATTTCAACAGAGAAAAGTAAACAAAGGACTTAACAAAAGAACAAACTTAGCCT	1140	100.0%	1485	100.0%	0	0	0	0	0	
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1261	CTGACAGTAGCTCTGGCAACTCCACACCATCTCATGCCAGAACATTCAAGAAC	1320	100.0%	1485	100.0%	0	0	0	0	0	
1261	CTGACAGTAGCTCTGGCAACTCCACACCATCTCATGCCAGAACATTCAAGAAC	1320	100.0%	1485	100.0%	0	0	0	0	0	
1321	CAAAAAAGGCAGCACAAACAGTGAAGGGTCTGGGACTAGCTGAAATGAAATATT	1380	100.0%	1485	100.0%	0	0	0	0	0	
1321	CAAAAAAGGCAGCACAAACAGTGAAGGGTCTGGGACTAGCTGAAATGAAATATT	1380	100.0%	1485	100.0%	0	0	0	0	0	
1381	ACATCAATCAACTGTGTAACCTAGGCAAGTCACCTAGCCACTTCTGGCTGGGACTAGCTGAAATGAAATATT	1440	100.0%	1485	100.0%	0	0	0	0	0	
1381	ACATCAATCAACTGTGTAACCTAGGCAAGTCACCTAGCCACTTCTGGCTGGGACTAGCTGAAATGAAATATT	1440	100.0%	1485	100.0%	0	0	0	0	0	
1441	TTTATCTAAATGAGGGTTATACTAAAAAAAGAAAAA	1485	100.0%	1485	100.0%	0	0	0	0	0	
1441	TTTATCTAAATGAGGGTTATACTAAAAAAAGAAAAA	1485	100.0%	1485	100.0%	0	0	0	0	0	
721	CGACTGTGTAACCTACCTGGCTGGATGCTGAGGGC	780	100.0%	1485	100.0%	0	0	0	0	0	
721	CGACTGTGTAACCTACCTGGCTGGATGCTGAGGGC	780	100.0%	1485	100.0%	0	0	0	0	0	
781	TACTCGAACCTAATCCAGAACAACTTACCTGGCTGGATGCTGAGGGC	840	100.0%	1485	100.0%	0	0	0	0	0	
781	TACTCGAACCTAATCCAGAACAACTTACCTGGCTGGATGCTGAGGGC	840	100.0%	1485	100.0%	0	0	0	0	0	

RESULT 3
S-10-254-869-1
Sequence 1, Application US/10254869
Publication No. US20030027307A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al

Qy 841 ATATGAATGATAAACTGGATGGCAGTTCAAGAAGGGCTCATTCAGGTTTCAATT 900
 Db 841 ATATGAATGATAAACTGGATGGCAGTTCAAGAAGGGCTCATTCAGGTTTCAATT 900
 Qy 901 CTAATAAAGGCAGGCTGAATTGTGATCCTACCTTGAACTTGAGGAATGATTGGAGT 960
 Db 901 CTAATAAAGGCAGGCTGAATTGTGATCCTACCTTGAACTTGAGGAATGATTGGAGT 960
 Qy 961 CCAAACCTCTACATAAGAAAAGGGTCTGGCAAAAGGAAGGGATATGAGGAAT 1020
 Db 961 CCAAACCTCTACATAAGAAAAGGGTCTGGCAAAAGGAAGGGATATGAGGAAT 1020
 Qy 1021 GCGATTCTCTACAGACATGTCTCTCAAGGCCAGAGGGTTCA 1080
 Db 1021 GCGATTCTCTACAGACATGTCTCTCAAGGCCAGAGGGTTCA 1080
 Qy 1081 TAATTTCAACAGAGAAAAGTAAACAGGGACTTAAACAAAGACAACC 1140
 Db 1081 TAATTTCAACAGAGAAAAGTAAACAGGGACTTAAACAAAGACAACC 1140
 Qy 1141 TGGAAACAAACCCAAAGCCCCAACGGTGGGCTCAGAATAACACTT 1200
 Db 1141 TGGAAACAAACCCAAAGCCCCAACGGTGGGCTCAGAATAACACTT 1200
 Qy 1201 ATGTCCTCTTCTGGGACAATCTCATGCCAGAACCTTCTAAAGAAAAG 1260
 Db 1201 ATGTCCTCTTCTGGGACAATCTCATGCCAGAACCTTCTAAAGAAAAG 1260
 Qy 1261 CTGACAGTAGCTCTGCCACACACCATGACTTAAAGTGAATATATT 1320
 Db 1261 CTGACAGTAGCTCTGCCACACACCATGACTTAAAGTGAATATATT 1320
 Qy 1321 CAAAAAAGGCAGCACAAACACAGTGAAGGGTCTGGCCCTGAAGTCATTTC 1380
 Db 1321 CAAAAAAGGCAGCACAAACACAGTGAAGGGTCTGGCCCTGAAGTCATTTC 1380
 Qy 1381 ACATCAATCAACTGTGTGATCTAGAGGAAGTCACTTAGCCACTTCTGTGCTTTACTTTA 1440
 Db 1381 ACATCAATCAACTGTGTGATCTAGAGGAAGTCACTTAGCCACTTCTGTGCTTTACTTTA 1440
 Qy 1441 TTATCTAAATGAGGGTTTACTAAAAAA 1485
 Db 1441 TTATCTAAATGAGGGTTTACTAAAAAA 1485
 RESULT 4
 US-10-410-764-100
 ; Sequence 100, Application US/10410764
 ; Publication No. US20040005664A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Meyers, Rachel E.
 ; APPLICANT: MacBeth, Kyle J.
 ; APPLICANT: Curtis, Rory A.J.
 ; APPLICANT: Rudolph-Owen, Laura A.
 ; APPLICANT: Weich, Nadine S.
 ; APPLICANT: Olandt, Peter J.
 ; APPLICANT: Tsai, Fong-Ying
 ; APPLICANT: Kapeller-Libermann, Rosana
 ; APPLICANT: Carroll, Joseph M.
 ; CURRENT FILING DATE: 2003-04-10
 ; PRIOR APPLICATION NUMBER: US/10/410,764
 ; PRIOR FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: US 09/924,358
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: US 10/350,553
 ; PRIOR FILING DATE: 2003-01-24
 US 60/351,572
 ; PRIOR APPLICATION NUMBER: US 60/351,572
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: US 09/966,614
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US 60/238,054
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: US 10/281,094
 ; PRIOR FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: US 60/347,815
 ; PRIOR FILING DATE: 2001-10-29
 ; PRIOR APPLICATION NUMBER: US 10/076,535
 ; PRIOR FILING DATE: 2002-02-15
 ; PRIOR APPLICATION NUMBER: US 60/269,440
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 136
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 100
 ; LENGTH: 1281
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (49) ... (1239)
 ; US-10-410-764-100
 Query Match 82.7%; score 1228.6; DB 16; Length 1281;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1231; Conservative 0; Mismatches 4; Indels 0;
 Gaps 0;
 Qy 1 CCATGGGAGGGAAACACTTCAAGAAAACCACCAACTGTTGATGAAATGAAGATGTCAACT 60
 Db 47 CCATGGGAGGCCAACACTTCAAGAAAACCACCAACTGTTGATGAAATGAAGATGTCAACT 106
 Qy 61 TTGACCACTTTGAAATTTCGAGCCATTGGGAAGGCAGTTTGGGGAGGTCTGCATGT 120
 Db 107 TTGACCACTTTGAAATTTCGAGCCATTGGGAAGGCAGTTTGGGAAGGTCTGCATGT 166
 Qy 121 TACAGAAGAAATGATAACCAAGAAGATGTGCCCATTGAAAGTACATGAAATAAACAAAAGTGC 180
 Db 167 TACAGAAGAAATGATAACCAAGAAGATGTGCCCATTGAAAGTACATGAAATAAACAAAAGTGC 226
 Qy 181 TGGAGGCCAATGAAATTGAGGTGAGAAATGCTTCAAGGAACCTCCAGATCATGGAGGCTCTGGAGC 240
 Db 227 TGGAGGCCAATGAAATTGAGGTGAGAAATGCTTCAAGGAACCTCCAGATCATGGAGGCTCTGGAGC 285
 Qy 241 ACCCTTCTCTGTTAATTGTTGAGTAAATGTTCAAGGAGACATGTTCATGGTGG 300
 Db 287 ACCCTTCTCTGTTAATTGTTGAGTAAATGTTCAAGGAGACATGTTCATGGTGG 346
 Qy 301 TGGACCTCTGCTGCTGGAGACCTGCTGGTATCACCTGCAACAGAACGTCACCTCAAGG 360
 Db 347 TGGACCTCTGCTGCTGGAGACCTGCTGGTATCACCTGCAACAGAACGTCACCTCAAGG 406
 Qy 361 AGAAAACAGTGAAGCTCTTCATCTGTGAGTCTCTGCTGGAGACCTGCAGAAC 420
 Db 407 AGAAAACAGTGAAGCTCTTCATCTGTGAGTCTCTGCTGGAGACCTGCAGAAC 466
 Qy 421 AGGGCATCATTCACAGGAGATGAAAGCCTGACAATATTTCATCTGAGAAACATGGGACAG 480
 Db 467 AGGGCATCATTCACAGGAGATGAAAGCCTGACAATATTTCATCTGAGAAACATGGGACAG 526
 Qy 541 TGGCTGGCACAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGGAGGCT 600
 Db 587 TGGCTGGCACAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAGGAGGAGGCT 646
 Qy 601 ATTCCCTTGTGCTGTTGACTGGCTGCTGCTGGAGTGTGAGGGCATATGAAACTGTGCTGAGGGCC 660
 Db 647 ATTCCCTTGTGCTGTTGACTGGCTGCTGCTGGAGTGTGAGGGCATATGAAACTGTGCTGAGGGCC 706

Qy	661	GGAGACCGTATCATATTGCTCCAGTACTTCCAGGAAGCAAGAAATTGTACACAGTTTGAGA	720
D _b	707	GGAGACCGTATCATATTGCTCCAGTACTTCCAGGAAGAAATTGTACACAGTTTGAGA	766
Qy	721	CGACTGTTGTAACCTACCCCTTCTGCCTGGTCAGGAATTGGTCAACTTCTTAAAGGC	780
D _b	767	CGACTGTTGTAACCTACCCCTTCTGCCTGGTCAGGAATTGGTCAACTTCTTAAAGGC	826
Qy	781	TACTCGAACCTAATCCAGAACCGATTCTCAGTTATCTGATGTCCAGAACCTCCCGT	840
D _b	827	TACTCGAACCTAATCCAGAACCGATTCTCAGTTATCTGATGTCCAGAACCTCCCGT	886
Qy	841	ATATGAATGATAATAACTGGGATGCGAGTTTCAAGAAGGGCTCATTCCAGGTTTCAATT	900
D _b	887	ATATGAATGATAATAACTGGGATGCGAGTTTCAAGAAGGGCTCATTCCAGGTTTCAATT	946
Qy	901	CTAATAAGGCCAGGCTGAATTGTGATCCTTGAACCTTGAAGGAAATGATTGGAGT	960
D _b	947	CTAATAAGGCCAGGCTGAATTGTGATCCTTGAACCTTGAAGGAAATGATTGGAGT	1006
Qy	961	CCAAACCTCTACATAAGAAAAAAAGGGCTGGCAAAGAACGGGAAGGATATGAGGAAT	1020
D _b	1007	CCAAACCTCTACATAAGAAAAAAAGGGCTGGCAAAGAACGGGAAGGATATGAGGAAT	1066
Qy	1021	GCGATTCTCTCAGACATGTCTCAAGAGCACCTTGACTCTGTCCAGAACGGTTCA	1080
D _b	1067	GCGATTCTCTCAGACATGTCTCAAGAGCACCTTGACTCTGTCCAGAACGGTTCA	1126
Qy	1081	TAATTTCAACAGAGAAAAAGTAAACGGGACTTTAACAAAAGAACCAATCTAGCCT	1140
D _b	1127	TAATTTCAACAGAGAAAAAGTAAACGGGACTTTAACAAAAGAACCAATCTAGCCT	1186
Qy	1141	TGGAAACAAACCAAGACCCACAAGGTGAGGATGGTCAAATAACAAACTTGTAAAGGCCTC	1200
D _b	1187	TGGAAACAAACCAAGACCCACAAGGTGAGGATGGTCAAATAACAAACTTGTAAAGGCCTC	1246
Qy	1201	ATGTCTCTCTGGACAATCTCATGCCAGAAC 1235	
D _b	1247	ATGTCTCTCTGGACAATCTCATGCCAGAAC 1281	

PESCHITT 5

Qy	241	ACCCFTCCCTGGTAAAGGAAAGACATGGTCAAGGAGG 300
Db	642	ACCCTTCCCTGGTTAATTGTGGTATTCTTCCAGATGAGGAACATGGTCAAGG 701
Qy	301	TGGACCTCCTGCTGGAGACCTGGCTTATCCTGCAAACAGAACGCTCAACTTCAGG 360
Db	702	TGGACCTCCTGCTGGAGACCTGGCTTATCCTGCAAACAGAACGCTCAACTTCAGG 761
Qy	361	AGAAAACAGTGAAGCTCTTCACTCTGTGAGCTCATGGCCCTGACTACACTGCAGAACCC 420
Db	762	AGAAAACAGTGAAGCTCTTCACTCTGTGAGCTCATGGCCCTGACTACACTGCAGAACCC 821
Qy	421	AGGGCATCATTCAACAGGGATATGAAGGCCCTGACAATTATTACTTGACGAAACATGGGCACG 480
Db	822	AGGGCATCATTCAACAGGGATATGAAGGCCCTGACAATTATTACTTGACGAAACATGGGCACG 881
Qy	481	TGGCACATCACAGATTCAACATTGGCATGGCATGGCAGACACAGATTACACACAGATTACACACCA 540
Db	882	TGGCACATCACAGATTCAACATTGGCATGGCATGGCAGACACAGATTACACACCA 941
Qy	541	TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTGAGTCCAGAAAAAGGGAGGCGCT 600
Db	942	TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTGAGTCCAGAAAAAGGGAGGCGCT 1001
Qy	601	ATTCCCTTGCTGTTGACTGGTCCCTGGAGTGGCATATGAACTGGCTGAGGGCC 660
Db	1002	ATTCCCTTGCTGTTGACTGGTCCCTGGAGTGGCATATGAACTGGCTGAGGGCC 1061
Qy	661	GGAGACCCTGATCATATTGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTGAGA 720
Db	1062	GGAGACCCTGATCATATTGCTCCAGTACTTCCAGCAAGGAAATTGTACACACGTTGAGA 1121

QY 721 CGACTGTTGAACTTACCCCTGCGTCAAGGAATGGTCACTTCAAAGC 780
 Db 1122 CGACTGTTGAACTTACCCCTGCGTCAAGGAATGGTCACTTCAAAGC 1181
 QY 781 TACTGAACTTAATCCAGCAACGAACTTCAGTTATCTGATGTCAGGCT 840
 Db 1182 TACTGAACTTAATCCAGCAACGAACTTCAGTTATCTGATGTCAGGCT 1241
 QY 841 ATATGAATGATAAACTGGATGCAAGTTTCAGAAGAGGTCACTCCATT 900
 Db 1242 ATATGAATGATAAACTGGATGCAAGTTTCAGAAGAGGTCACTCCATT 1301
 QY 901 CTAATAAGGCAGGCTGAATTGTGATCCTACCTTGAACTTGGAGT 960
 Db 1302 CTAATAAGGCAGGCTGAATTGTGATCCTACCTTGAACTTGGAGT 1361
 QY 961 CCAAACCTCTACATAAGAAAAAGGGCTGGAAAGGAAGGATATGAGGAAT 1020
 Db 1362 CCAAACCTCTACATAAGAAAAAGGGCTGGAAAGGAAGGATATGAGGAAT 1421
 QY 1021 GCGATTCTCTCAGACATGTCCTCAAGGCACTTGACTCTGTCAGAAGGTTCA 1080
 Db 1422 GCGATTCTCTCAGACATGTCCTCAAGGCACTTGACTCTGTCAGAAGGTTCA 1481
 QY 1081 TAATTTCACAGAGAAAAGTAAACAGGACTTTAACAAAGACAACCAATCTAGCCT 1140
 Db 1482 TAATTTCACAGAGAAAAGTAAACAGGACTTTAACAAAGACAACCAATCTAGCCT 1541
 QY 1141 TGGAACAAACCCAAAGGCAACAGGTGAGGATCCTCAGAATAACACTTGAA 1193
 Db 1542 TGGAACAAACCCAAAGGCAACAGGTGAGGATCCTCAGAATAACACTTGAA 1594

RESULT 6
 US-10-182-243-1
 ; Sequence 1, Application US/10182243
 ; Publication No. US20040048310A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PLOWMAN, GREGORY D.
 ; APPLICANT: WHYTE, DAVID
 ; APPLICANT: MANNING, GERARD
 ; APPLICANT: SUDARSANAM, SUCHA
 ; APPLICANT: MARTINEZ, RICARDO
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
 ; TITLE OF INVENTION: ENZYMES
 ; FILE REFERENCE: 038602/1366
 ; CURRENT APPLICATION NUMBER: US/10/182,243
 ; CURRENT FILING DATE: 2003-07-07
 ; PRIOR APPLICATION NUMBER: PCT/US01/02337
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1594
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-182-243-1

Query Match 80.0%; Score 1188.2; DB 13; Length 1594;
 Best Local Similarity 99.7%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATGGGAGGAAACCTCAAGAAAACCACCAAGTGGTTGATGAAAGATGTCACT 60
 Db 402 CCATGGGAGGAAACCTCAAGAAAACCACCAAGTGGTTGATGAAAGATGTCACT 461
 QY 61 TTGACCACTTGAATTGGAGCCATTGGAAAGGCAGTTGGGAGGTCTGCATTG 120
 Db 462 TTGACCACTTGAATTGGAGCCATTGGAAAGGCAGTTGGGAGGTCTGCATTG 521
 QY 121 TACAGNAGAATGATACCAAGAAGATGTACGGCAATGAACTGAAATAACAAAGTGGC 180
 Db 522 TACAGNAGAATGATACCAAGAAGATGTACGGCAATGAACTGAAATAACAAAGTGGC 581

RESULT 7
 US-10-288-798-44
 ; Sequence 44, Application US/10288798

; GENERAL INFORMATION:

; APPLICANT: BANDMAN, Olga; NGUYEN, Daniel B;

; APPLICANT: WALIA, Narinder K; HAFALIA, April J.A.;

; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;

; APPLICANT: GURURAJAN, Rajagopal; DING, Li;

; APPLICANT: PATTERSON, Chandra; YUE, Henry;

; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;

; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;

; APPLICANT: LU, Yan; ISON, Craig H.;

; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;

; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;

; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;

; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;

; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;

; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;

; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil

; TITLE OF INVENTION: HUMAN KINASES

; FILE REFERENCE: PI-0209 USA

; CURRENT APPLICATION NUMBER: US/10/288,798

; CURRENT FILING DATE: 2002-11-01

; PRIOR APPLICATION NUMBER: PCT/US01/27219

; PRIOR FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: US 60/240,542

; PRIOR FILING DATE: 2000-10-13

; PRIOR APPLICATION NUMBER: US 60/238,389

; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: US 60/236,499

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: US 60/234,902

; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: US 60/232,654

; PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: US 60/231,357

; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: US 60/229,873

; PRIOR FILING DATE: 2000-08-31

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PERL program

; SEQ ID NO 44

; LENGTH: 1594

; TYPE: DNA

; ORGANISM: Homo sapiens

; NAME/KEY: misc_feature

; FEATURE:

; OTHER INFORMATION: Incyte ID No. US20030207299A1 7946584CB1

; US-10-288-798-44

; Query Match

; Best Local Similarity

; Mismatches

; Pred. No.

; Indels

; Gaps

; 0;

; Matches

; 1190;

; Conservative

; 0;

; Mismatches

; 0;

; Gaps

; 0;

; US-10-288-798-44

; Score: 1188.2;

; DB: 16;

; Length: 1594;

; ;

; ;

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; ;

; ;

; ;

; 702 TGGACCTCCTGGGTGGAGAACCTGCACACTTCACCTCAAGG 761

; 361 AAGAAAACAGTGAAAGCTCTTCATCTGTGAGCTACCTGCAGAAC 420

; 762 AAGAAAACAGTGAAAGCTCTTCATCTGTGAGCTACCTGCAGAAC 821

; 421 AGGCCATATTCAACGGGATATGAAGCAGTGGCAG 480

; 822 AGGCCATATTCAACGGGATATGAAGCAGTGGCAG 881

; 481 TGCACATCACAGATTCAACATGCTGGCATGCTGCCAGAGTACCA 540

; 882 TGCACATCACAGATTCAACATGCTGGCATGCTGCCAGAGTACCA 941

; 541 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTAGCTGAGGGCC 600

; 942 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTAGCTGAGGGCC 1001

; 601 ATTCCCTTGCTGTTGACTTGGTCCCTGGAGTGAACCTGAGGGCC 660

; 1002 ATTCCCTTGCTGTTGACTTGGTCCCTGGAGTGAACCTGAGGGCC 1061

; 661 GGAGACCGTATCATATTGCTCAGTACTTCCAGCAAGGAATTGTAACACGTTGAGA 720

; 1062 GGAGACCGTATCATATTGCTCAGTACTTCCAGCAAGGAATTGTAACACGTTGAGA 1121

; 721 CGACTGTGTAACTTACCCCTTGCTGGTCAAGGAATGGTGTCACTTCTAAAGC 780

; 1122 CGACTGTGTAACTTACCCCTTGCTGGTCAAGGAATGGTGTCACTTCTAAAGC 1181

; 781 TACTCGAACCTTAATCAGACCAACGATTTCAGTTATCTGATGTCAGTTCCAGAACACTTCCCCT 840

; 1182 TACTCGAACCTTAATCAGACCAACGATTTCAGTTATCTGATGTCAGTTCCAGAACACTTCCCCT 1241

; 841 ATATGAATGATAAAACTTGGATGTCAGTTTCAGTTCCAGAACATTTGAGT 900

; 1242 ATATGAATGATAAAACTTGGATGTCAGTTTCAGTTCCAGAACATTTGAGT 1301

; 901 CTAATAAAGGCAGGTGAATTGTGATCCTAACCTTTGAGTAAATGATTGGAGT 960

; 1302 CTAATAAAGGCAGGTGAATTGTGATCCTAACCTTTGAGTAAATGATTGGAGT 1361

; 961 CCAAACCTCTACATAAGAAAAAAAGCGTCTGGCAAGGACCTGACTCTGTCCAGMAGGAGTTCA 1020

; 1422 CGGATTCTCTCAGACATGTCTCTTCAGACATGTCTCTCAGACAGCTGTCCAGRAAGGTTCA 1481

; 1081 TAATTTCACAGAGAAAGTAAACAGGGAATTAAACAAAGCAACCAAAATCTAGCCT 1140

; 1482 TAATTTCACAGAGAAAGTAAACAGGGAATTAAACAAAGCAACCAAAATCTAGCCT 1541

; 1141 TGGAACAAACCAAGAACCCACAAGGTGAGATGGTCAGAATAACAACTGTAA 1193

; 1542 TGGAACAAACCAAGAACCCACAAGGTGAGATGGTCAGAATAACAACTGTAA 1594

; RESULT 8

; US-09-841-683-10

; Sequence 10, Application US/09841683

; Patent No. US20020081600A1

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; NEPMICHY, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Wade, D. Wade

; TITLE OF INVENTION: No. US20020081600A1

; FILE REFERENCE: LEX-0167-USA

; 301 TGGACCTCCTGGTGGAGACCTGCACACTTCACCTCAAGG 360

CURRENT APPLICATION NUMBER: US/09/841, 683
 CURRENT FILING DATE: 2001-04-24
 PRIOR APPLICATION NUMBER: US 60/199, 499
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: US 60/201, 227
 PRIOR FILING DATE: 2000-05-01
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 10
 LENGTH: 1191
 TYPE: DNA
 ORGANISM: homo sapiens
 US-09-841-683-10

Query Match 79.9%; Score 1186.2; DB 9; Length 1191;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGGAGCGAAACTTCAGAAAACCACCACTTCAAGGAAACACTTCAGATGTCAACTTT 62
 Db 1 ATGGAGGCCAACACTTCAGAAAACCACCACTGTTGTGAAATGAGATGTCAACTT 60

Qy 63 GACCAACTTTGAAATTGGCAGGCCATTGGGAAAGGCAGTTTGGGGAGGETCTGCAATGTA 122
 Db 61 GACCAACTTTGAAATTGGCAGGCCATTGGAAAGGGAGTTTGGGAAGGTCTGCAATGTA 120

Qy 123 CAGAAGAAATGATAACCAAGAAGATGTGGCAATGAAAGTACATGAAATAAACAAAAAGTGGTG 182
 Db 121 CAGAAGAAATGATAACCAAGAAGATGTGAAATGAGTACATGAAATAAACAAAAAGTGGTG 180

Qy 183 GAGGCACATGAAAGTGAGAAATGTCTTAAGGAACCTCCAGATCATGGCAGGGTCTGGAGCAC 242
 Db 181 GAGGCCAAATGAGAATGCTTCAAGGAACCTCCAGATCATGGCAGGGTCTGGAGCAC 240

Qy 243 CCTTCTGGTTAATTGTGGTATTCTTCCAAGATGAGGAAGACATGTCATGGTGGTG 302
 Db 241 CCTTCTGGTTAATTGTGGTATTCTTCCAAGATGAGGAAGACATGTCATGGTGGTG 300

Qy 303 GACCTCCTGGGAGACCTGCTTACCTGCAAAGAACGTCACTTCAGGAA 362
 Db 301 GACCTCCTGGGAGACCTGCTTACCTGCAAAGAACGTCACTTCAGGAA 360

Qy 363 GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCAATGGCCCTGGACTACCTGAGAACCCAG 422
 Db 361 GAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCAATGGCCCTGGACTACCTGAGAACCCAG 420

Qy 423 CGCATCATTCAACAGGATATGAGCCTGACAATAATTACTTGACGAACATGGCACTGGCACTGG 482
 Db 421 CGCATCATTCAACGGGATATGAGCTGGTCAATGGCAACATGGCACTGGCACTGG 480

Qy 483 CACATCACAGATTCAACATTGCTGAGCTGGTCAATGGCCCTGGAGACAGATTACCATG 542
 Db 481 CACATCACAGATTCAACATTGCTGAGCTGGTCAATGGCAACATGGCACTGGCACTGG 540

Qy 543 GCTGGCACCAAGGCCTTACATGGCACCTGAGATGTTAGCTCAGCTCAGAAAGGAGGCTAT 602
 Db 541 GCTGGCACCAAGGCCTTACATGGCACCTGAGATGTTAGCTCAGCTCAGAAAGGAGGCTAT 600

Qy 603 TCCTTGTGTGACTGGTGGGAGTGAACGGCATATGAAACTGCTGAGAGGCCGG 662
 Db 601 TCCTTGTGTGACTGGTGGGAGTGAACGGCATATGAAACTGCTGAGAGGCCGG 660

Qy 663 AGACCGTATCATATTGCTTCCAGTACTCCAGCAAGGAATGGTACACAGCTTGGACAG 722
 Db 661 AGACCGTATCATATTGCTTCCAGTACTCCAGCAAGGAATGGTACACAGCTTGGACAG 720

Qy 723 ACTGTTGTAACCTAACCTTGTGCTGACTGGTCACTCTTAAAGCTA 782
 Db 721 ACTGTTGTAACCTAACCTTGTGCTGACTGGTCACTCTTAAAGCTA 780

Qy 783 CTCGAACCTTAATCCAGAACCAACGATTCTGCTTCAAGAACCTCCCGTAT 842
 Db 781 CTCGAACCTTAATCCAGAACCAACGATTCTGCTTCAAGAACCTCCCGTAT 840

RESULT 9
 US-10-410-764-102
 ; Sequence 102, Application US/10410764
 ; Publication No. US20040005664A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Meyers, Rachel E.
 ; APPLICANT: MacBeth, Kyle J.
 ; APPLICANT: Curtis, Rory A.J.
 ; APPLICANT: Rudolph-Owen, Laura A.
 ; APPLICANT: Weich, Nadine S.
 ; APPLICANT: Olandt, Peter J.
 ; APPLICANT: Tsai, Pong-Ying
 ; APPLICANT: Kapeller-Liebermann, Rosana
 ; APPLICANT: Carroll, Joseph M.
 ; APPLICANT: Carroll, Joseph M.
 ; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
 ; TITLE OF INVENTION: 58764, 62113, 32144, 32235, 23565,
 ; TITLE OF INVENTION: 13305, 14911, 86216,
 ; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
 ; FILE REFERENCE: MPI03-0520MNTM
 ; CURRENT APPLICATION NUMBER: US/10/410,764
 ; CURRENT FILING DATE: 2003-04-10
 ; PRIOR APPLICATION NUMBER: US 09/924,358
 ; PRIOR FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: US 60/229,300
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: US 10/350,553
 ; PRIOR FILING DATE: 2003-01-24
 ; PRIOR APPLICATION NUMBER: US 60/351,572
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: US 09/966, 614
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US 60/238,054
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: US 10/281, 094
 ; PRIOR FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: US 60/347, 815
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 136
 ; SOFTWARE: FastSBQ for Windows Version 4.0
 ; SEQ ID NO 102
 ; LENGTH: 1191
 ; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: (1)...(1191)
; LOCATION: US-10-410-764-102

Query Match 79.8%; Score 1184.6; DB 16; Length 1191;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1187; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ATGGCAGGAAACACTTCAAGAAAACCACCACTGTTGTGAAATGAAGATGTCAACTTT 62
Db 1 ATGGAGCCAACACTTCAAGAAAACCACCACTGTTGTGAAATGAAGATGTCAACTTT 60

Qy 63 GACCACTTGAATTTCGAGCCATTGGAAAGGCCAGTTGGGAGGTCTGCATTGTA 122
Db 61 GACCACTTGAATTTCGAGCCATTGGAAAGGCCAGTTGGGAGGTCTGCATTGTA 120

Qy 123 CAGAAGATGATAACCAAGAAGATGTGCCCATGAAAGTACATGAAATAAACAAAGTGGTGT 182
Db 121 CAGAAGAATGATAACCAAGAAGATGTACATGAAATAAACAAAGTGGTGT 180

Qy 183 GAGGGCAATGAAAGTGGAAACTCCAGATCATGAGGGTCTGGAGCAC 242
Db 181 GAGGGCAATGAAAGTGGAAACTCCAGATCATGAGGGTCTGGAGCAC 240

Qy 243 CCTTTCTGGTTAATTGGGTATTCCCAAGAATGGAAACATGTTCATGGTGGTG 302
Db 241 CCTTTCTGGTTAATTGGGTATTCCCAAGAATGGAAACATGTTCATGGTGGTG 300

Qy 303 GACCTCCCTGCTGGAGACCTGTTATCACCTGAAACAGAACGTCCACTTCAAGGAA 362
Db 301 GACCTCTGCTGGAGACCTGTTATCACCTGAAACAGAACGTCCACTTCAAGGAA 360

Qy 363 GAAACAGTGAAGCTCTCATCTGTGAGCTGCTGGACTACCTGCGAAACCCAG 422
Db 361 GAAACAGTGAAGCTCTCATCTGTGAGCTGCTGGACTACCTGCGAAACCCAG 420

Qy 423 CGCATCATTCAAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACCGTG 482
Db 421 CGCATCATTCAAGGGATATGAAGCCTGACAATATTTTACTTGACGAACATGGGCACCGTG 480

Qy 483 CACATCACAGATTCAACATTTGCTGGCATGCTGCCAGGGAGAACAGATTACCATG 542
Db 481 CACATCACAGATTCAACATTTGCTGGCATGCTGCCAGGGAGAACAGATTACCATG 540

Qy 543 GCTGGCACCAGCTTACATGGCACCTGAGATGTCAAGTCAGCTCCAGGAGGGTAT 602
Db 541 GCTGGCACCAGCTTACATGGCACCTGAGATGTCAAGTCAGCTCCAGGAGGGTAT 600

Qy 603 TCCTTTCGCTGGTGACTGGTCCCTGGAGTGAAGGCATATGAACGTGCTGAGAGGGCGG 662
Db 601 TCCTTTCGCTGGTGACTGGTCCCTGGAGTGAAGGCATATGAACGTGCTGAGAGGGCGG 660

Qy 663 AGACCGTATCATATTGCTCCAGTACTTCAGAACAGGAATTGTACACAGTTGAGACG 722
Db 661 AGACCGTATCATATTGCTCCAGTACTTCAGAACAGGAATTGTACACAGTTGAGACG 720

Qy 723 ACTGTTGTAACATTACCCCTTCTGCCTGGTCAAGGAATGGTGTCACTTCAAGGCTA 782
Db 721 ACTGTTGTAACATTACCCCTTCTGCCTGGTCAAGGAATGGTGTCACTTCAAGGCTA 780

Qy 783 CTCGAACTTAATCCAGACCAACGATTTCCTCAGTTATCTGATGTTCTCCCGTAT 842
Db 781 CTCGAACTTAATCCAGACCAACGATTTCCTCAGTTATCTGATGTTCTCCCGTAT 840

Qy 843 ATGAAFTGATAAACTGGATGCACTTTCAGAAGAGGCTCATTCAGTTTCAATTCCT 902
Db 841 ATGAAFTGATAAACTGGGATGCAATTGTGATCCTAACCTTTCAGGAAATGGTGTCC 900

Qy 903 AATAAAGGAGGCTGAATTGTGATCCTAACCTTTCAGGAAATGGTGTCC 962
Db 901 AATAAAGGAGGCTGAATTGTGATCCTAACCTTTCAGGAAATGGTGTCC 960

Qy 963 AACCTCTACATAAGAAAAAAGCGTCTGGCAAAAGAGGAAAGGATATGAGGAATGTC 1022
Db 961 AACCTCTACATAAGAAAAAAGCGTCTGGCAAAAGAGGAAAGGATATGAGGAATGTC 1020

Qy 1023 GATTCTCTCAGACATGCTCTTCAAGAGCACCTGACTCTGTCAGGAGGTCTATA 1082
Db 1021 GATTCTCTCAGACATGCTCTTCAAGAGCACCTGACTCTGTCAGGAGGTCTATA 1080

Qy 1083 ATTTCACAGAGAAAAGTAACAGGGACCTTAACAAAGAACCAAATCTAGGCTTG 1142
Db 1081 ATTTCACAGAGAAAAGTAACAGGGACCTTAACAAAGAACCAAATCTAGGCTTG 1140

Qy 1143 GAACAAACCAAGGCCAACAAAGTGGTCAGAATAACACTTGTA 1193
Db 1141 GAACAAACCAAGGCCAACAAAGTGGTCAGAATAACACTTGTA 1191

RESULT 10
US-09-841-683-12
; Sequence 12 , Application US/09841683
; Patent No. US20020081600A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1675
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-841-683-12

Query Match 78.3%; Score 1162.6; DB 9; Length 1675;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CCATGGGAGCGAACACTTCAAGAAAACCACCACTGTTGATGAAATGAAGATGTCAACT 60
Db 411 CCATGGGAGGCCAACACTTCAAGAAAACCACCACTGTTGATGAAATGAAGATGTCAACT 470

Qy 61 TTGACCACTTGAATTTCGCGAGCCATTGGAAAAGGCAGTTGGGGAGGTCTGCATRG 120
Db 471 TTGACCACTTGAATTTCGCGAGCCATTGGAAAAGGCAGTTGGGGAGGTCTGCATRG 530

Qy 121 TACAGAAGGAATGATAACCAAGAAGATGTGCGCAATGAAAGTACATGAATAAAAGTGGG 180
Db 531 TACAGAAGGAATGATAACCAAGAAGATGTGCGCAATGAAAGTACATGAATAAAAGTGGG 590

Qy 181 TGGAGGCCAATGAAACTTCTCAAGGAACCTCCAGATCATGGGGTCTGGAGGC 240
Db 591 TGGAGGCCAATGAAACTTCTCAAGGAACCTCCAGATCATGGGGTCTGGAGGC 650

Qy 241 ACCCTTCTCTGGTATTCTCCAGAATGAGATGAGGAGCATGTTCATGGTGG 300
Db 651 ACCCTTCTCTGGTATTCTCCAGAATGAGATGAGGAGCATGTTCATGGTGG 710

Qy 301 TGGACCTCTGGTGGAGACCTCTGGTGGAGGAAATGTTGGACTTCACCTGCAAGG 360
Db 711 TGGACCTCTGGTGGAGGAAATGTTGGACTTCACCTGCAAGG 770

361 AAGAAACAGTGAAGCTCTTCATCTGGAGCTCATGGCCCTGGACTACCTGGAGAACCC 420
 771 AAGAAACAGTGAAGCTCTTCATCTGGAGCTCATGGCCCTGGACTACCTGGAGAACCC 830

421 AGGCATCATTCAACGGGATATGAAAGCCTGACATAATTTCATTTGACGAACATGGGCCAGC 480
 831 AGGCATCATTCAACGGGATATGAAAGCCTGACATAATTTCATTTGACGAACATGGGCCAGC 890

481 TGCACATCACAGATTCAACATTTGCTGGATGGTGGCCAGGGAGACACAGATTACCA 540
 891 TGCAATCACAGATTCAACATTTGCTGGATGGTGGCCAGGGAGACACAGATTACCA 950

541 TGGCTGGACCAAGCCTTACATGGCACCTGAGATGTTAGCTCCAGAAAAGGAGCGGT 600
 951 TGGCTGGACCAAGCCTTACATGGCACCTGAGATGTTAGCTCCAGAAAAGGAGCGGT 1010

601 ATTCTTGTGTTGACTTGGTCCAGTACTTCCAGCAAGGAAATTGACACAGTTTGAGA 660
 1011 ATTCTTGTGTTGACTTGGTCCAGTACTTCCAGCAAGGAAATTGACACAGTTTGAGA 1070

661 GGAGACCGTATCATATTCCGCTCCAGTACTTCCAGCAAGGAAATTGACACAGTTTGAGA 720
 1071 GGAGACCGTATCATATTCCGCTCCAGTACTTCCAGCAAGGAAATTGACACAGTTTGAGA 1130

721 CGACTTGTGTAACTTACCCCTCTGCCTGGTCAAGGAAATTGCTGCACTTCTAAAGGC 780
 1131 CGACTTGTGTAACTTACCCCTCTGCCTGGTCAAGGAAATTGCTGCACTTCTAAAGGC 1190

781 TACTCGAACCTTAATCCAGAACGATTTCAGTTCTCAAGGAAACTTCCCGT 840
 1191 TACTCGAACCTTAATCCAGAACGATTTCAGTTCTCAAGGAAACTTCCCGT 1250

841 ATATGAAATGATAATAACTGGATGCAAGTTCTCAAGAAGGGCTCATTCAGGTTTCATTTC 900
 1251 ATATGAAATGATAATAACTGGATGCAAGTTCTCAAGAAGGGCTCATTCAGGTTTCATTTC 1310

901 CTAATAAGGGCAGGCTGAATTGTGATCTACCTTGAACCTTGCAAGGAAATTGGAGT 960
 1311 CTAATAAGGGCAGGCTGAATTGTGATCTACCTTGAACCTTGCAAGGAAATTGGAGT 1370

961 CCAAACCTCTACATAAGAAAAAAAGGTCAGGAAAGGAAAGGAAAGGAAAT 1020
 1371 CCAAACCTCTACATAAGAAAAAAAGGTCAGGAAAGGAAAGGAAAT 1430

1021 GCGATTCTCTCAGACATGTTCTCAAGAGCACCTTGTGACTCTGTCCAGAAGGACTTC 1080
 1431 GCGATTCTCTCAGACATGTTCTCAAGAGCACCTTGTGACTCTGTCCAGAAGGAGTTCA 1490

1081 TAATTTCAACAGAGAAAAAGTAAACAGGGACTTTAACAAAGACAACAAATCTTAGCCT 1140
 1491 TAATTTCAACAGAGAAAAAGTAAACAGGGACTTTAACAAAGACAACAAATCTAGCCT 1550

1141 TGGAAACAAACCAAGGCAACAGGTGAGGTCAAGATAACA 1185
 1551 TGGAAACAAACCAAGGCAACAGGTGAGGTCAAGATAACA 1595

RESULT 11
 US-09-841-683-8
 Sequence 8, Application US/09841683
 Patent No. US20020081600A1
 GENERAL INFORMATION:
 APPLICANT: Hu, YI
 APPLICANT: Nepomnyichy, Boris
 APPLICANT: Wang, Xiaoming
 APPLICANT: Donoho, Gregory
 APPLICANT: Scoville, John
 APPLICANT: Walko, D. Wade
 TITLE OF INVENTION: No. US20020081600A1 Human Kinase Proteins and Polynucleotides E
 FILE REFERENCE: LEX-0167-USA
 CURRENT APPLICATION NUMBER: US/09/841,683
 CURRENT FILING DATE: 2001-04-24
 PRIOR APPLICATION NUMBER: US 60/199,499

QY ; PRIOR FILING DATE: 2000-04-25
 Db ; PRIOR APPLICATION NUMBER: US 60/201,227
 QY ; PRIOR FILING DATE: 2000-05-01
 Db ; NUMBER OF SEQ ID NOS: 12
 QY ; SOFTWARE: FastSEQ for Windows Version 4.0
 Db ; SEQ ID NO: 8
 QY ; LENGTH: 1224
 Db ; TYPE: DNA
 QY ; ORGANISM: homo sapiens
 Db ; US-09-841-683-8

Query Match 78.2%; Score 1160.6; DB 9; Length 1224;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1169; Conservatve 0; Mismatches 14; Indels 0; Gaps 0;

QY 3 ATGGGAGCGAACACTTCAGAAAAACCACAGTGTGATGAAAGATGTCAACTTT 62
 Db 1 ATGGGAGCCAACACTTCAGAAAAACCACAGTGTGATGAAAGATGTCAACTTT 60

QY 63 GACCACTTGAAATTGGAGCCATTGGAAAGGAGTTGGGGAGGTCTGCATTGTA 122
 Db 61 GACCACTTGAAATTGGAGCCATTGGAAAGGCAAGTTGGGAAAGGTCTGCATTGTA 120

QY 123 CAGAAGAATGATAACCAAGAAGATGTGGCAATGAAATAACAAAAAGTGCCTG 182
 Db 121 CAGAAGAATGATAACCAAGAAGATGTACGAAATGAAAGTCACTGAAATAACAAAAAGTGCCTG 180

QY 183 GAGGCGAAATGAAAGTGGAAATGCTTCAAGGAACCTCAGATCTGAGGGAC 242
 Db 181 GAGGCGAAATGAAAGTGGAAATGCTTCAAGGAACCTCAGATCTGAGGGAC 240

QY 243 CCTTTCTCTGGTTAATTGGTTATTCCCTCAAGATGAGGAACATGGTCATGGGGTG 302
 Db 241 CCTTCTCTGGTTAATTGGTTATTCCCTCAAGATGAGGAACATGGTCATGGGGTG 300

QY 303 GACCTCTGCTGGTGGAGACTCTGCCTGCTCATCCTCAAGGAACTCTCAAGGAA 362
 Db 301 GACCTCTGCTGGTGGAGACTCTGCCTGCTCATCCTCAAGGAACTCTCAAGGAA 360

QY 363 GAAAAGTGAAGCTCTCATCTGTGAGGTGGTCACTGGCCCTGGACTACCTGAGAACACAG 422
 Db 361 GAAAAGTGAAGCTCTCATCTGTGAGGTGGTCACTGGCCCTGGACTACCTGAGAACACAG 420

QY 423 CGCATCATTCAAGGGGATATGAGGCTCATGGCTGAAACATGGGCACCTG 482
 Db 421 CGCATCATTCAAGGGGATATGAGGCTCATGGCTGAAACATGGGCACCTG 480

QY 483 CACATCACAGATTCAACATGGCTGCGATGTCGCCCACGGGAGAACAGATTAACCCATG 542
 Db 481 CACATCACAGATTCAACATGGCTGCGATGTCGCCCACGGGAGAACAGATTAACCCATG 540

QY 543 GCTGGCACCAGGCTTACATGGCACCTGAGATGTTAGCTCAGGTCAGGAGGGCTAT 602
 Db 541 GCTGGCACCAGGCTTACATGGCACCTGAGATGTTAGCTCAGGTCAGGAGGGCTAT 600

QY 603 TCCTTGTGTRACTGGTGGACTCTGGAGTGAACGGCATATGAACTGCTGAGGGCCGG 662
 Db 601 TCCTTGTGTRACTGGTGGACTCTGGAGTGAACGGCATATGAACTGCTGAGGGCCGG 660

QY 663 AGACCGTATCATATTGCTCOAGTACTTCAGCAAGGAATTGTACACAGCTTGTGAGACG 722
 Db 661 AGACCGTATCATATTGCTCOAGTACTTCAGCAAGGAATTGTACACAGCTTGTGAGACG 720

QY 723 ACTGTTGTAACCTAACCTCTGGTCAAGGAAATGGTGTCACTCTTAAAGCTA 782
 Db 721 ACTGTTGTAACCTAACCTCTGGTCAAGGAAATGGTGTCACTCTTAAAGCTA 780

QY 783 CTCGAACCTTAATCAGACCAACGATTCTCTGAGTCAAGGAAATGGTGTCACTCTGGT 842
 Db 781 CTCGAACCTTAATCAGACCAACGATTCTCTGAGTCAAGGAAATGGTGTCACTCTGGT 840

QY 843 ATGAATGATAAAACTGGATGCAAGGAAATGGGATGCAAGGAAATGGGACCT 902

841	ATGAATGATAATAACTGGGATTCAGAACAGGGTCAATTCCAGGTTCATTCCT	900	Qy
903	ATAAAGGCAAGGCTGAATTGTGATCCTACCTTGAACCTGGATTTGGAGTCC	962	Db
901	ATAAAGGCAAGGCTGAATTGTGATCCTACCTTGAACCTGGATTTGGAGTCC	960	Qy
963	AAACCTCTACATAAGAAAAAGGCTGGCAAGGAAGGATAATGAGGAATATGC	1022	Db
961	AAACCTCTACATAAGAAAAAGGCTGGCAAGGAAGGATAATGAGGAATACCA	871	Qy
1023	GATTCTCTCAGACATGTCCTTCAGAGCACCTGACTCTGTCCAGAAGGGTCA	1082	Db
1021	GATTCTCTCAGACATGTCCTTCAGAGCACCTGACTCTGTCCAGAAGGGTCA	1020	Qy
1083	ATTTCAACAGAGAAAAGTAACAGGGACTTTAACAAAGACAACCAAATCTAG	1142	Db
1081	ATTTCAACAGAGAAAAGTAACAGGGACTTTAACAAAGACAACCAAATCTAG	1140	Qy
1143	GAACAAACCAAAAGGCAACAAATGGACAATAACA 1185	Db	Qy
1141	GAACAAACCAAAAGGCAACAAATGGACAATAACA 1183	Db	Db
RESULT 12	US-10-108-260A-231		
	; Sequence 231, Application US/10108260A		
	; Publication No. US20040005560A1		
	; GENERAL INFORMATION:		
	; APPLICANT: HELIX RESEARCH INSTITUTE		
	; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA		
	; FILE REFERENCE: H1-A0106		
	; CURRENT APPLICATION NUMBER: US/108-260A		
	; CURRENT FILING DATE: 2002-03-27		
	; NUMBER OF SEQ ID NOS: 5458		
	; SOFTWARE: PatentIn Ver. 2.1		
	; SEQ ID NO 231		
	; LENGTH: 2063		
	; TYPE: DNA		
	; ORGANISM: Homo sapiens		
	; US-10-108-260A-231		
Qy	Query Match 69.3%; Score 1029.4; DB 16; Length 2063;		
Db	Best Local Similarity 99.4%; Pred. No. 2.2e-300; Mismatches 6; Indels 0; Gaps 0;		
Qy	1 CCATGGGAGCGAACACTTCAGAAAACCACCTCAAGAAATGAGTGTCAACT	60	Qy
Db	332 CCATGGGAGCCAACACTTCAGAAAACCACCTCAAGAAATGAGTGTCAACT	391	Db
Qy	61 TTGACCACTTGAAATTGGAGCCATTGGAAAGGCAGTTGGGAGGTCTGCATTG	120	Qy
Db	392 TTGACCACTTGAAATTGGAGCCATTGGAAAGGCAGTTGGGAGGTCTGCATTG	451	Db
Qy	121 TACAGAAAGATGATAACCAAGAAAGATGTGGCAATGAAGTACATGAATAAACAAAGTGG	180	Qy
Db	452 TACAGAAAGATGATAACCAAGAAAGATGTGGCAATGAAGTACATGAATAAACAAAGTGG	511	Db
Qy	181 TGAGGGCGCAATGAAAGTGGAAATTGTCTCAAGGAACCTCCAGGGTCTGGAGC	240	Qy
Db	512 TGAGGGCGCAATGAAAGTGGAAATTGTCTCAAGGAACCTCCAGGGTCTGGAGC	571	Db
Qy	241 ACCCTTCCCTGGTTAATTGTGGTATTCTTCAAGATGAGGAAGACATGTTCATGGTGG	300	Qy
Db	572 ACCCTTCCCTGGTTAATTGTGGTATTCTTCAAGATGAGGAAGACATGTTCATGGTGG	631	Db
Qy	301 TGGACCTCTGGAGGAGACCTGGTATTCAACCTGCAACAGAACGTCACACTCAAGG	360	Qy
Db	632 TGGACCTCTGGAGGAGACCTGGTATTCAACCTGCAACAGAACGTCACACTCAAGG	691	Db
Qy	Query Match 45.3%; Score 672.8; DB 13; Length 678;		
Db	Best Local Similarity 99.7%; Pred. No. 1.2e-192; Mismatches 2; Indels 0; Gaps 0;		
Qy	Matches 674; Conservative 0; Matches 0; Gaps 0;		
Db	441 ATGAAAGCCTGACAAATTTACTTGTGACGAAACATGGCACGTCACATCACAGATTCAAC 500		

US-09-841-683-6

Query Match 44.2%; Score 656.2; DB 9; Length 711;

Best Local Similarity 99.5%; Pred. No. 1.3e-187; Mismatches 3; Indels 0; Gaps 0;

Matches 658; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGGGAGGAAACACTTCAAGAAAACCACCAAGCTTAC 622

Db 1 ATGGGAGGAAACACTTCAAGAAAACCACCAAGCTTAC 60

Qy 63 GACCACTTGAAATTTCGAGGCCATTGGGAAAGGAAGCTGTTGCATTGTA 122

Db 1 ATGGGAGGAAACACTTCAAGAAAACCACCAAGCTTAC 60

Qy 61 GACCACTTGAAATTTCGAGGCCATTGGGAAAGGAAGCTGTTGCATTGTA 120

Db 121 ATGGCACCTGAGATGTTCAAGTCCAGAAAGGGCAGGCTTACCTTGGCTGTTGACTGG 620

Qy 621 TGGTCCCTGGAGTGAAGTGAAGGGCATATGAAGCTGCTGAGGGAGACCGTACATATTCG 680

Db 181 TGGTCCCTGGAGTGAAGTGAAGGGCATATGAAGCTGCTGAGGGAGACCGTACATATTCG 240

Qy 681 TCCAGTACTTCAGCAAGGAATTGTACACACGTTTGAGAAGACTGTTGAACTTACCT 740

Db 241 TCCAGTACTTCAGCAAGGAATTGTACACACGTTTGAGAAGCTGTTGAACTTACCT 300

Qy 741 TCTGCCCTGGTCAACAGGAATGGTCACTTCAGAACTTAATCCAGAC 800

Db 301 TCTGCCCTGGTCAACAGGAATGGTCACTTCAGAACTTAATCCAGAC 360

Qy 801 CAACGATTTCAGTGTCCAGAACTTCCGTATAATGAATGATAACTGG 860

Db 361 CAACGATTTCAGTGTCCAGAACTTCCGTATAATGAATGATAACTGG 420

Qy 861 GATGCCAGTTCAGTGTCCATTCAGGTTTCATTCAGGTTCAACCTTACATGGCTGAAT 920

Db 421 GATGCCAGTTCAGTGTCCATTCAGGTTCAACCTTACATGGCTGAAT 480

Qy 921 TGTGATCCCTACCTTCAAGAAGGGCTCATTCAGGTTCAACCTTACATAGAAA 980

Db 481 TGTGATCCCTACCTTCAAGAAGGGCTCATTCAGGTTCAACCTTACATAGAAA 540

Qy 981 AAAAAGCGTCTGAGAACCTTGAAGGAATGATTGGAGTCACAGCATGT 1040

Db 541 AAAAAGCGTCTGAGAACCTTGAAGGAAGGGATAATGAGGAATTCAGACATGT 600

Qy 1041 CTTCTTCAGAGGCACCTTGACTCTGTTCCAGAAGGGAGTCATAATTTCAGAGAAA 1100

Db 601 CTTCTTCAGAGGCACCTTGACTCTGTTCCAGAAGGGAGTCATAATTTCAGAGAAA 660

Qy 1101 GTAAACAGGGACTTTA 1116

Db 661 GTAAACAGGGACTGTA 676

RESULT 14 US-09-841-683-6

Sequence 6, Application US/09841683

Patent No. US20020081600A1

GENERAL INFORMATION:

APPLICANT: Hu, Yi

APPLICANT: Nepomnichy, Boris

APPLICANT: Wang, Xiaoming

APPLICANT: Donoho, Gregory

APPLICANT: Scoville, John

APPLICANT: Walké, D. Wade

TITLE OF INVENTION: NO. US20020081600A1 Human Kinase Proteins and Polynucleotides

FILE REFERENCE: LEX-0167-USA

CURRENT APPLICATION NUMBER: US/09/841,683

CURRENT FILING DATE: 2001-04-24

PRIOR APPLICATION NUMBER: US 60/199,499

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 60/201,227

PRIOR FILING DATE: 2000-05-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6 LENGTH: 711

TYPE: DNA

ORGANISM: homo sapiens

RESULT 15 US-09-841-683-4

Sequence 4, Application US/09841683

Patent No. US20020081600A1

GENERAL INFORMATION:

APPLICANT: Hu, Yi

APPLICANT: Nepomnichy, Boris

APPLICANT: Wang, Xiaoming

APPLICANT: Donoho, Gregory

APPLICANT: Scoville, John

APPLICANT: Walké, D. Wade

TITLE OF INVENTION: No. US20020081600A1 Human Kinase Proteins and Polynucleotide:

FILE REFERENCE: LEX-0167-USA

CURRENT APPLICATION NUMBER: US/09/841,683

CURRENT FILING DATE: 2001-04-24

PRIOR APPLICATION NUMBER: US 60/199,499

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US 60/201,227

PRIOR FILING DATE: 2000-05-01

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; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 678
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-4

Query Match      44.1%; Score 655.2; DB 9; Length 678;
Best Local Similarity 99.5%; Pred. No. 2.6e-187;
Matches 657; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db          1 ATGGGAGCCAAACACTTCAAGAAAACCACAGTTGTTGATGAAATGAAGATGTCAACTTT 62
Qy          3 ATGGGAGCGAACACTTCAAGAAAACCACAGTTGTTGATGAAATGAAGATGTCAACTTT 62
Db          1 ATGGGAGCCAAACACTTCAAGAAAACCACAGTTGTTGATGAAATGAAGATGTCAACTTT 60
Qy          63 GACCACTTTGAAATTTCGGAGGCCATTGGAAAGGCCAGTTTGGGAGCTTGCATTGTA 122
Db          61 GACCACTTTGAAATTTCGGAGGCCATTGGAAAGGCCAGTTTGGGAGCTTGCATTGTA 120
Qy          123 CAGAAGAATGATAACCAAGAAGATGTGCCAATGAAAGTACATGAAATAACAAAAGTGGTG 182
Db          121 CAGAAGAATGATAACCAAGAAGATGTGAACTGCAATGAAAGTACATGAAATAACAAAAGTGGTG 180
Qy          183 GAGGCCAATGAACTGAGAAATTGTGAACTTCAAGGAACCTCCAGATCATGGAGGCTCTGGAGCAC 242
Db          181 GAGGCCAATGAACTGAGAAATTGTGAACTTCAAGGAACCTCCAGATCATGGAGGCTCTGGAGCAC 240
Qy          243 CCTTTCTGGTTAATTGTGGTATTCCCTTCAAGATGGAAAGACATGTTCATGGTGGTG 302
Db          241 CCTTTCTGGTTAATTGTGGTATTCCCTTCAAGATGGAAAGACATGTTCATGGTGGTG 300
Qy          303 GACCTCTGGCTGGGGAGACCTGGTATCACCTGAAACAGAACGTCCACTTCAAGGAA 362
Db          301 GACCTCTGGCTGGGGAGACCTGGTATCACCTGAAACAGAACGTCCACTTCAAGGAA 360
Qy          363 GAAACAGTGAAGGCTCTCATCTGTGAGCTGGTCATGGCCCTGGAACACTGGCAGAACACAG 422
Db          361 GAAACAGTGAAGGCTCTCATCTGTGAGCTGGTCATGGCCCTGGAACACTGGCAGAACACAG 420
Qy          423 CGCATCATTCAAGGGATATGAAGCCTGACAATAATTACTTGACGAACATGGCAGACGTG 482
Db          421 CGCATCATTCAAGGGATATGAAGCCTGACAATAATTACTTGACGAACATGGCAGACGTG 480
Qy          483 CACATCACAGATTCAACATTGCTGCGATGCTGCCAGGGAGACACATTACCACTG 542
Db          481 CACATCACAGATTCAACATTGCTGCGATGCTGCCAGGGAGACACATTACCACTG 540
Qy          543 GCTGGCACCAAGGCTTACATGGCACCTGAGATGTTCAAGTCAGCTCCAGAAAGGAGGGCTAT 602
Db          541 GCTGGCACCAAGGCTTACATGGCACCTGAGATGTTCAAGTCAGCTCCAGAAAGGAGGGCTAT 600
Qy          603 TCCTTGCTGTTGACTGGTGTCCCTGGGAGTGAAGGCATATGAACACTGCTGAGGGCGG 662
Db          601 TCCTTGCTGTTGACTGGTGTCCCTGGGAGTGAAGGCATATGAACACTGCTGAGGGCGG 660

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Search completed: June 27, 2004, 00:23:55
Job time : 504 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 20:58:26 ; Search time 95 Seconds
 (without alignments)
 8674.759 Million cell updates/sec

Title: US-10-667-442-1
 Perfect score: 1485
 Sequence: 1 ccatggggcgaaaccttca.....taaaaaaaaaaaaaaaa 1485

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents NA:
 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq: *
 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq: *
 6: /cgn2_6/ptodata/2/ina/backFiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1485	100.0	1485	4	US-09-801-876B-1	Sequence 1, Appli
2	1485	100.0	1485	4	US-10-254-869-1	Sequence 1, Appli
3	1186.2	79.9	1191	4	US-09-841-683-10	Sequence 10, Appli
4	1162.6	78.3	1675	4	US-09-841-683-12	Sequence 12, Appli
5	1160.6	78.2	1224	4	US-09-841-683-8	Sequence 8, Appli
6	656.2	44.2	711	4	US-09-841-683-6	Sequence 6, Appli
7	655.2	44.1	678	4	US-09-841-683-4	Sequence 4, Appli
8	481.6	32.4	1257	4	US-09-799-875-15	Sequence 15, Appli
9	481.6	32.4	1826	4	US-09-799-875-13	Sequence 13, Appli
10	466.8	31.4	1864	4	US-09-819-607-1	Sequence 1, Appli
11	363.4	24.5	148567	4	US-09-801-876B-3	Sequence 3, Appli
12	363.4	24.5	148567	4	US-10-254-869-3	Sequence 3, Appli
13	132.6	8.9	1008	4	US-09-394-455-14	Sequence 14, Appli
14	132.6	8.9	2549	3	US-09-819-607-3	Sequence 3, Appli
15	132.6	8.9	2549	4	US-09-394-455-5	Sequence 5, Appli
16	132.6	8.9	2608	4	US-09-394-455-35	Sequence 35, Appli
17	132	8.9	1619	4	US-09-394-455-14	Sequence 14, Appli
18	122.6	8.3	25603	4	US-09-819-607-3	Sequence 3, Appli
19	120.4	8.1	1498	4	US-09-509-902A-6	Sequence 6, Appli
20	120.4	8.1	1961	4	US-09-509-902A-15	Sequence 15, Appli
21	120.4	8.1	2204	1	US-08-221-817-12	Sequence 12, Appli
22	120.4	8.1	2204	1	US-08-454-439-12	Sequence 12, Appli
23	120.4	8.1	2204	5	PCT-US94-10487-12	Sequence 12, Appli
24	120.4	8.1	2206	1	US-08-221-817-10	Sequence 10, Appli
25	120.4	8.1	2206	1	US-08-454-439-10	Sequence 10, Appli
26	120.4	8.1	2206	5	PCT-US94-10487-10	Sequence 10, Appli
27	120.4	8.1	2848	3	US-08-464-954A-2	Sequence 2, Appli

RESULT 1						
US-09-801-876B-1						
;	Sequence 1, Application	US/09801876B	;	Patent No. 6492155	;	GENERAL INFORMATION:
;	APPLICANT: YE, Jane et al	;	;	FILE REFERENCE: CL001160	;	TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
;	CURRENT APPLICATION NUMBER: US/09/801,876B	;	;	CURRENT FILING DATE: 2001-03-09	;	NUMBER OF SEQ ID NOS: 8
;	SOFTWARE: FastSEQ for Windows Version 4.0	;	;	SEQ ID NO 1	;	LENGTH: 1485
;	TYPE: DNA	;	;	ORGANISM: Human	;	US-09-801-876B-1

Query Match						
Best Local Similarity						
;	100.0%	Score 1485;	DB 4;	Length 1485;	;	Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;	100.0%	Pred. No. 0;	;	;	;	;
;	1	CCATGGGGCGAAACACTTCAGAAAATGAAAGTGTCAACT	60	;	Qy	;
;	1	CCATGGGGCGAAACACTTCAGAAAATGAAAGTGTCAACT	60	;	Db	;
;	1	TTGACCATTTGAAATTGGAGGCCATTGGAAAGGCAGTTGGGAGGTCTGCATTG	120	;	Qy	;
;	1	TTGACCATTTGAAATTGGAGGCCATTGGAAAGGCAGTTGGGAGGTCTGCATTG	120	;	Db	;
;	121	TACAGAAAGAATGATAACCAAGAAAGTGTGCCAATGAAGTACATGAAATAAACAAAGTGC	180	;	Qy	;
;	121	TGGAGCGCAATGAACTCCAGATCATGGGGCTCTGGAGGC	300	;	Db	;
;	181	TGGACCTTCTGGTTAATTGTGGTATTCCAGATGTTCTGGAGC	240	;	Qy	;
;	181	ACCCRTCTGTAAATTGTGGTATTCCAGATGTTCTGGAGC	300	;	Db	;
;	181	TGGACCTTCTGGTTAATTGTGGTATTCCAGATGTTCTGGAGC	240	;	Qy	;
;	301	TGGACCTTCTGGTTAATTGTGGTATTCCAGATGTTCTGGAGC	360	;	Db	;
;	301	ACCCRTCTGTAAATTGTGGTATTCCAGATGTTCTGGAGC	360	;	Qy	;
;	361	AGAAAACAGTGAAGCTCTCATGTGGACTACCTGGAGAAC	420	;	Db	;

RESUME²
US-10-254-869-1
Sequence 1, Application US/10254869
Patent No. 6653117
GENERAL INFORMATION:
APPLICANT: YB, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CL001160DIV
CURRENT APPLICATION NUMBER: US/10/254, 869
CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1485
TYPE: DNA
ORGANISM: Human
US-10-254-869-1

Query Match Score 1485; DB 4; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCATGGGAGCGAACACTTCAAGAAAAACCACCTTCAGGTGTTGATGAAAATGAAGATGTCAACT	60
Db	1	CCATGGGAGCGAACACTTCAAGAAAAACCACCTTCAGGTGTTGATGAAAATGAAGATGTCAACT	60
Qy	61	TTGACCACATTGAAATTTCGGCAGGCCATTGGAAAGGCAGTTTGGGAGGGTCTGCAATRG	120
Db	61	TTGACCACATTGAAATTTCGGCAGGCCATTGGAAAGGCAGTTTGGGAGGGTCTGCAATRG	120
Qy	61	TACAGAGAATGATACCAAGAAGATGTGCCATTGAAACTCATGAAATAAACAAAAGTGG	180
Db	61	TACAGAGAATGATACCAAGAAGATGTGCCATTGAAACTCATGAAATAAACAAAAGTGG	180
Qy	181	TGGAGGCCAATGAAAGTGTGAAATTCTCAAGGAACATCGCAGGTTCTGGAGC	240
Db	181	TGGAGGCCAATGAAATTCTCAAGGAACATCGCAGGTTCTGGAGC	240
Qy	241	ACCCTTCCCTGGTTAATTGTGTTTCAAGGAAACTCCAGATCATGGCTCTGGAGC	300
Db	241	ACCCTTCCCTGGTTAATTGTGTTTCAAGGAAACTCCAGATCATGGCTCTGGAGC	300
Qy	301	TGGACCTCCCTGGCTGTTAATTGTGTTTCAAGGAAACTCCAGATCATGGCTCTGGAGC	360
Db	301	TGGACCTCCCTGGCTGTTAATTGTGTTTCAAGGAAACTCCAGATCATGGCTCTGGAGC	360
Qy	361	AAGAAACAGTGAAAGCTCTTCAGATGAGCTGGCTCATGGCCCTGGACTACCTGCAAGACC	420
Db	361	AAGAAACAGTGAAAGCTCTTCAGATGAGCTGGCTCATGGCCCTGGACTACCTGCAAGACC	420
Qy	421	AGGGCATTCATTCAAGGGATAATGAAGGCTGACAATTTACTTGACGAACATGGGCAGC	480
Db	421	AGGGCATTCATTCAAGGGATAATGAAGGCTGACAATTTACTTGACGAACATGGGCAGC	480
Qy	481	TGCACATCACAGATTTCACATTGCACTGGGAGCATGGTCAAGTTCAGCTTACACCA	540
Db	481	TGCACATCACAGATTTCACATTGCACTGGGAGCATGGTCAAGTTCAGCTTACACCA	540
Qy	541	TGGCTGCCACCAAGCCTTACATGGTGAAGTGTCAAGCTCCAGGAGGAGGAGGCT	600
Db	541	TGGCTGCCACCAAGCCTTACATGGTGAAGTGTCAAGCTCCAGGAGGAGGAGGCT	600
Qy	601	ATTCCCTTGGTGTGACTGGTCCCTCAGTACTTCAGGAAAGGAATTTGTACACAGTTGAGA	720
Db	601	ATTCCCTTGGTGTGACTGGTCCCTCAGTACTTCAGGAAAGGAATTTGTACACAGTTGAGA	720
Qy	661	GGAGACCGTATCATATTTCGCTCCAGTACTAGGAAAGGGTATACTAAAAAAAGAAAAA	720
Db	661	GGAGACCGTATCATATTTCGCTCCAGTACTAGGAAAGGGTATACTAAAAAAAGAAAAA	720

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSBQ For Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-841-683-10

Query Match Score 1186.2; DB 4; Length 1191;
Best Local Similarity 99.7%; Pred. No. 0; Gaps 0;
Matches 1188; Conservative 0; Mismatches 3; Indels 0;

Start	End	Sequence
3	62	ATGGGAGCGAACACTTCAAGAAAACCACAGTGTCCAGAACTTCCCGT
1	60	ATGGGAGCCAACACTTCAAGAAAACCACAGTGTCCAGAACTTCCCGT
63	122	GACCACTTGAATTTGGAGGGCATTGGGAAGGGCAGTTTGATGAAATGAGATGTCAACTTT
1	61	GACCACTTGAATTTGGAGGGCATTGGGAAGGGCAGTTTGATGAAATGAGATGTCAACTTT
123	182	CAGAAGAATGATAACCAAGAAGATGTGCGCAATGAACTGAGATTAACAAAAGTGCCTGCGGTG
121	180	CAGAAGAATGATAACCAAGAAGATGTGCGCAATGAACTGAGATTAACAAAAGTGCCTGCGGTG
183	242	GAGGGCAATGAAGTGAAGAATGGTCTCAAGGAACACTCCAGATCATGGCAGGGTCTGGAGCAC
181	240	GAGGGCAATGAAGTGAAGAATGGTCTCAAGGAACACTCCAGATCATGGCAGGGTCTGGAGCAC
243	302	CCTTTCCTGGTTAATTGTGGTATTCTCCAAAGATGAGGAAGACATGTTCATGGTGGTG
241	300	CCTTTCCTGGTTAATTGTGGTATTCTCCAAAGATGAGGAAGACATGTTCATGGTGGTG
303	362	GACCTCTGGCTGGGAGACCTGGCTTATCACCTGGCAACAGAACGTCACCTCAAGGAA
301	360	GACCTCTGGCTGGGAGACCTGGCTTATCACCTGGCAACAGAACGTCACCTCAAGGAA
363	422	GAAACAGTGAAGCTCTCATCTGTGAAGCTGGACTACCTGAGAACTTCAAGGAA
361	420	GAAACAGTGAAGCTCTCATCTGTGAAGCTGGACTACCTGAGAACTTCAAGGAA
423	482	CGCATATTCAAGGGATATGAAAGAACATGGCAAGCTTCAAGGAA
421	480	CGCATATTCAAGGGATATGAAAGAACATGGCAAGCTTCAAGGAA
483	542	CACATCACAGATTCAACATTGCTGGGATGCTGGCTGGGAGAGCACAGTCAACCATG
481	540	CACATCACAGATTCAACATTGCTGGGATGCTGGCTGGGAGAGCACAGTCAACCATG
543	602	GCTGGGACCAAGCCTTACATGGCACCTGAGTGGGGACTTCTGGGAGGCTAT
541	600	GCTGGGACCAAGCCTTACATGGCACCTGAGTGGGGACTTCTGGGAGGCTAT
603	662	TCCRTTGGCTGTTGACTGGCACCTGAGATGGTCCAGAAAGGGAGGGCTAT
601	660	TCCRTTGGCTGTTGACTGGCACCTGAGATGGTCCAGAAAGGGAGGGCTAT
663	722	AGACCGTATCATATTGCTCCAGTACTCCAGAACGAAATTGTAACACGTTGAGACG
661	720	AGACCGTATCATATTGCTCCAGTACTCCAGAACGAAATTGTAACACGTTGAGACG
723	902	ACTGTTGTAACTTACCCCTTCTGCTGGTCAAGGAATGGTGTCAACTTCTGAGT
721	900	ACTGTTGTAACTTACCCCTTCTGCTGGTCAAGGAATGGTGTCAACTTCTGAGT
783	843	CTCGAACCTTAATCCAGACCAACGATTTCCAGAACTTCCAGTTTCAAGGAA
781	841	CTCGAACCTTAATCCAGACCAACGATTTCCAGAACTTCCAGTTTCAAGGAA
843	962	ATGAATGATAAAACTGGGATGCAATTGTGATCTACCTTGAACATTGGAGTC
841	962	ATGAATGATAAAACTGGGATGCAATTGTGATCTACCTTGAACATTGGAGTC
903	962	AATAAAGGCAGGGTGAATTGTGATCTACCTTGAACATTGGAGTC

RESULT 3
S-09 841-683-10
Sequence 10, Application US/09841683
Patent No. 6617147
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
APPLICANT: Wang, Xiaoming
APPLICANT: Donoho, Gregory
APPLICANT: Scoville, John
APPLICANT: Walk, D. Wade
TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
FILE REFERENCE: LEX-0167-USA
CURRENT APPLICATION NUMBER: US/09/841, 683
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 60/199, 499
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 60/201, 227
PRIOR FILING DATE: 2000-05-01

RESULT 4
US-09-841-683-12
Sequence 12; Application US/09841683
Patent No. 6617147
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
APPLICANT: Wang, Xiaoming
APPLICANT: Donoho, Gregory
APPLICANT: Scoville, John
APPLICANT: Walk, D. Wade
TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
FILE REFERENCE: LEX-0167-USA
CURRENT APPLICATION NUMBER: US/09/841,683
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 60/199,499
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 60/201,227
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1675
TYPE: DNA
ORGANISM: homo sapiens
US-09-841-683-12

Query Match 78.3%; Score 1162.6; DB 4; Length 1675;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 CCATGGGGAACACTTCAAGAAACCCAGTGTGATGAAATGAAAGATGTCACT 60
Db 411 CCATGGGCAACACTTCAAGAAACCCAGTGTGATGAAATGAAAGATGTCACT 470

Qy 61 TTGACCACTTGAATTTCGAGCAATTGGAAAGGCAGTTGGGGAGGTCTGCATTG 120
Db 471 TTGACCACTTGAATTTCGAGCAATTGGAAAGGCAGTTGGGGAGGTCTGCATTG 530

Qy 121 TACAGAAGAATGATACCAAGGAAGATGTGGCAATGAAAGTACATGAATAACAAAGTGCG 180
Db 531 TACAGAAGAATGATACCAAGGAAGATGTACATGAATAACAAAGTGCG 590

Qy 181 TGGAGCGCAATGAAAGTCCAGGAACCTCCAGATCATGCAAGGGTCTGGAGC 240
Db 591 TGGAGCGCAATGAAAGTCCAGGAACCTCCAGATCATGCAAGGGTCTGGAGC 650

Qy 241 ACCCTTTCTGGTTAATTCTGGTAATTCTGGTCAAGGAACATGGTCTGGAGC 300
Db 651 ACCCTTTCTGGTTAATTCTGGTCAAGATGAGCAACTGGTCTGGAGC 710

Qy 301 TGGACCTCTGGTGGAGACCTGGTTATCACCTGCAACAGAACGGTCCACTTAAGG 360

Db 711 TGGACCTCTGGTGGAGACCTGGTTATCACCTGCAACAGAACGGTCCACTTAAGG 770
Qy 361 AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGGCCTGGACTACCTGGCAACCC 420
Db 771 AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGGCCTGGACTACCTGGCAACCC 830

Qy 421 AGGCATATTCAAGGGATATGAAAGCTGACAATAATTACTTGAGGAACATGGGCAAG 480
Db 831 AGGCATATTCAAGGGATATGAAAGCTGACAATAATTACTTGAGGAACATGGGCAAG 890

Qy 481 TGCAATCACAGATTCAACATTGCTGCAATGGCACCTTGAGCTGGCCAGGGACACAGATTACCCA 540
Db 891 TGCAATCACAGATTCAACATTGCTGCAATGGCACCTTGAGCTGGCCAGGGACACAGATTACCCA 950

Qy 541 TGGCTGGCACCAGCCTTACATGGCACCTGAGATGTTCAAGCTCCAGAAAAGGAGCAGGCT 600
Db 951 TGGCTGGCACCAGCCTTACATGGCACCTTGAGATGTTCAAGCTCCAGAAAAGGAGCAGGCT 1010

Qy 601 ATTCTTGTGTTGACTCTGGAGTGAAGCTGGCCATATGAAACTGCTGAGAGGCC 660
Db 1011 ATTCTTGTGTTGACTCTGGCCATATGAAACTGCTGAGAGGCC 1070

Qy 661 GGAGACCGTATCATATTGCTCCAGTACTTCCAGTGGAAATTGTACACAGTTTGAGA 720
Db 1131 CGACTGTGTTGAACTTACCCCTCTGGCTCACAGGAAATGGTCACTTAAAGGC 1190

Qy 781 TACTCGAACCTAATCCAGACCAACGATTTCCTCAGTATCTGATGTCAGAAACTTCCGGT 840
Db 1191 TACTCGAACCTAATCCAGACCAACGATTTCCTCAGTATCTGATGTCAGAAACTTCCGGT 1250

Qy 721 CGACTGTGAACTTACCCCTCTGGCTCACAGGAAATTGCTGTCACCTTAAAGGC 780
Db 1131 CGACTGTGTTGAACTTACCCCTCTGGCTCACAGGAAATGGTCACTTAAAGGC 1190

Qy 841 ATATGAACTGATAAAACTGGGATGCAAGTTTTCAGAAGAGGCTCATTCAGGTTTCATTC 900
Db 1251 ATATGAACTGATAAAACTGGGATGCAAGTTTTCAGAAGAGGCTCATTCAGGTTTCATTC 1310

Qy 901 CTAATAAGGAGGCTGAAATTGTGATCCTACCTTTGAACTTGAGGAATGTGTTGGAGT 960
Db 1311 CTAATAAGGAGGCTGAAATTGTGATCCTACCTTTGAACTTGAGGAATGTGTTGGAGT 1370

Qy 961 CCAAACCTCTACATAAGAAAMAAGGTTGGCAAAAGAAGGAAGGGATAAGGAAT 1020
Db 1371 CCAAACCTCTACATAAGAAAAAAGGTTGGCAAAAGAAGGAAGGGATAAGGAAT 1430

Qy 1021 GCGATTCTCTCAAGACATGTTCTTCAGAGGACCTTCAAGAGGAGCTGTCAGCT 1080
Db 1431 GCGATTCTCTCAAGACATGTTCTTCAGAGGACCTTCAAGAGGAGCTGTCAGCT 1490

Qy 1081 TAATTTCAACAGGAAAGGAAAGGAAACGTTAACAAAGACAACCAATCTAGCT 1140
Db 1491 TAATTTCAACAGGAAAGGAAACGTTAACAAAGACAACCAATCTAGCT 1550

Qy 1141 TGGAAACAAACCAAGGACCCAAAGGAAACGGTGGAGGTGGTCAAGATAACA 1185
Db 1551 TGGAAACAAACCAAGGACCCAAAGGAAACGGTGGAGGTGGTCAAGATAACA 1595

RESULT 5
US-09-841-683-8
Sequence 8; Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Walk, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683

CURRENT FILING DATE: 2001-04-24
 / PRIOR APPLICATION NUMBER: US 60/199,499
 / PRIOR FILING DATE: 2000-04-25
 / PRIOR APPLICATION NUMBER: US 60/201,227
 / PRIOR FILING DATE: 2000-05-01
 / NUMBER OF SEQ ID NOS: 12
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 8
 / LENGTH: 1224
 / TYPE: DNA
 / ORGANISM: homo sapiens
 US-09-841-683-8

Query Match Score 1160.6; DB 4; Length 1224;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 3 ATGGGAGCGAAACACTTCAGAAAACCAGTGTGTGATGAAATGAACTTT 62
 Db 1 ATGGGAGCCAAACACTTCAGAAAACCAGTGTGTGATGAAATGAACTTT 60

Qy 63 GACCACTTTGAATTTGGGAGCCATTGGAAAGGCCAGTTGGGAGGTCTGCATTGTA 122
 Db 61 GACCACTTTGAATTTGGGAGCCATTGGAAAGGCCAGTTGGGAGGTCTGCATTGTA 120

Qy 123 CAGAAGAATGATAACCAAGAAGATGTGCCAACATGAACTACATGATAAACAAAGTGGCTG 182
 Db 121 CAGAAGAATGATAACCAAGAAGATGTACGAAAGTACATGATAAACAAAGTGGCTG 180

Qy 183 GAGCCGAATGAAACTGAGAAACTCCAGATCATGCCAGGTCTGGAGCAC 242
 Db 181 GAGCCGAATGAAACTGAGAAACTCCAGATCATGCCAGGTCTGGAGCAC 240

Qy 243 CCTTTCTGGTTAATTGTGTGATTCCCTTCAAGATGAGGAGACATGTTCATGGTGTG 302
 Db 241 CCTTTCTGGTTAATTGTGTGATTCCCTTCAAGATGAGGAGACATGTTCATGGTGTG 300

Qy 303 GACCTCCTGGCTGAACTGGCTCTCATCTGTGAGCTGTGCTATGGCCTGACTACCTGCAGAACAG 362
 Db 301 GACCTCCTGGCTGAACTGGCTCTCATCTGTGAGCTGTGCTATGGCCTGACTACCTGCAGAACAG 360

Qy 363 GAAACAGTGAACTGAGCTCTCATCTGTGAGCTGTGCTATGGCCTGACTACCTGCAGAACAG 422
 Db 361 GAAACAGTGAACTGAGCTCTCATCTGTGAGCTGTGCTATGGCCTGACTACCTGCAGAACAG 420

Qy 423 CGCATCATTCAAGGGATATGAAAGCCTGACAATATTTACTTGACGAACATGGCACGTG 482
 Db 421 CGCATCATTCAAGGGATATGAAAGCCTGACAATATTTACTTGACGAACATGGCACGTG 480

Qy 483 CACATCACAGATTCAACATGCTGCCAACATGCTGCCAACATGCTGCCAACATG 542
 Db 481 CACATCACAGATTCAACATGCTGCCAACATGCTGCCAACATGCTGCCAACATG 540

Qy 543 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAAGTCCAGAAAAGGAGCAGGTAT 602
 Db 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAAGTCCAGAAAAGGAGCAGGTAT 600

Qy 603 TCCRTTGCTGTTGACTGGTGTCCCTGGAGTGACGGCATATGAACCTGCTGAGGGCGG 662
 Db 601 TCCRTTGCTGTTGACTGGTGTCCCTGGAGTGACGGCATATGAACCTGCTGAGGGCGG 660

Qy 663 AGACCGTATCATATTGCTCAGTACTCCAGCAAGGAATTGTACACAGCTTGGAGACG 722
 Db 661 AGACCGTATCATATTGCTCAGTACTCCAGCAAGGAATTGTACACAGCTTGGAGACG 720

Qy 723 ACTGTGTAACCTACCTTCTGCTGGTCACTTAAAGCTA 782
 Db 721 ACTGTGTAACCTACCTTCTGCTGGTCACTTAAAGCTA 780

Qy 783 CTCGAACCTAATCCAGACCAAGGATTCTCAAGGAACTTCCCGTAT 842
 Db 781 CTCGAACCTAATCCAGACCAAGGATTCTCAAGGAACTTCCCGTAT 840

Qy 963 AACCCCTCATAGAGAAAAAGGAAAGGATGAGGAAATGAGGAAATTCG 1022
 Db 961 AACCTCTACATAGAAAAAGGAAAGGATGAGGAAATTCG 1020

Qy 1023 GATTCTCTCAGACATGTCTTCAAGAGGCACCTGACTCTGTCAGAAGGAGTTCTATA 1082
 Db 1021 GATTCTCTCAGACATGTCTTCAAGAGGCACCTGACTCTGTCAGAAGGAGTTCTATA 1080

Qy 1083 ATTTCACAGAGAAAGTAAACAGGACTTTAACAAAAGACAACCAAATCTAGCCTTG 1142
 Db 1081 ATTTCACAGAGAAAGTAAACAGGACTTTAACAAAAGACAACCAAATCTAGCCTTG 1140

Qy 1143 GAACAAACCAAGAACCCACAAGTGTGAGGTCTGAGATAACA 1185
 Db 1141 GAACAAACCAAGAACCCACAAGTGTGACAAATGGACA 1183

RESULT 6
 US-09-841-683-6
 ; Sequence 6, Application US/09841683
 ; Patent No. 6617147
 ; GENERAL INFORMATION:
 / APPLICANT: Hu, Yi
 / NEPOMNICHY, Boris
 / APPLICANT: Wang, Xiaoming
 / APPLICANT: Donoho, Gregory
 / APPLICANT: Scoville, John
 / APPLICANT: Walk, D. Wade
 ; TITLE OF INVENTION: No. 6617147 e1 Human Kinase Proteins and Polynucleotides Encoding
 ; FILE REFERENCE: LEX-0167-USA
 ; CURRENT APPLICATION NUMBER: US 09/841,683
 ; CURRENT FILING DATE: 2001-04-24
 ; PRIOR APPLICATION NUMBER: US 60/199,499
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: US 60/201,227
 ; PRIOR FILING DATE: 2000-05-01
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 6
 ; LENGTH: 711
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-841-683-6
 ; Query Match Score 656.2; DB 4; Length 711;
 ; Best Local Similarity 99.5%; Pred. No. 3.5e-197;
 ; Matches 658; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATGGGAGCGAAACTCAAGAAAACCAGCTTGGAGCTTGGCATTTGCAACTTT 62
 Db 1 ATGGGAGCCAAACACTTCAGAAAAGGAGCTTGGCATTTGCAACTTT 60

Qy 63 GACCACTTGAAATTGGTGTGTTGACTACCTGCTGAGCTACCTGCAGAACAG 122
 Db 61 GACCACTTGAAATTGGTGTGTTGACTACCTGCTGAGCTACCTGCAGAACAG 120

Qy 123 CAGAAGAATGATAACCAAGAAGATGTGCCAACATGAACTACATGATAAACAAAGTGGCTG 182
 Db 121 CAGAAGAATGATAACCAAGAAGATGTACGAAAGTACATGATAAACAAAGTGGCTG 180

Qy 183 GAGCCGAATGAAACTGAGAAACTCCAGATCATGCCAGGTCTGGAGCAC 242
 Db 181 GAGCCGAATGAAACTGGCTCTCATCTGTGAGCTGTGCTATGGCCTGACTACCTGCAGAACAG 240

Qy 243 CCTTTCTGGTTAATTGTGTGATTCCCTTCAAGATGAGGAGACATGTTCATGGTGTG 302
 Db 241 CCTTTCTGGTTAATTGTGTGATTCCCTTCAAGATGAGGAGACATGTTCATGGTGTG 300

Qy 303 GACCTCCTGGCTGAACTGGCTCTCATCTGTGAGCTGTGCTATGGCCTGACTACCTGCAGAACAG 362
 Db 301 GACCTCCTGGCTGAACTGGCTCTCATCTGTGAGCTGTGCTATGGCCTGACTACCTGCAGAACAG 360

Qy 363 GAAACAGTGAACTGAGCTCTCATCTGTGAGCTGTGCTATGGCCTGACTACCTGCAGAACAG 422
 Db 361 GAAACAGTGAACTGGCTCTCATCTGTGAGCTGTGCTATGGCCTGACTACCTGCAGAACAG 420

Qy 423 CGCATCATTCAAGGGATATGAAAGCCTGACAATATTTACTTGACGAACATGGCACGTG 482
 Db 421 CGCATCATTCAAGGGATATGAAAGCCTGACAATATTTACTTGACGAACATGGCACGTG 480

Qy 483 CACATCACAGATTCAACATGCTGCCAACATGCTGCCAACATGCTGCCAACATG 542
 Db 481 CACATCACAGATTCAACATGCTGCCAACATGCTGCCAACATGCTGCCAACATG 540

Qy 543 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAAGTCCAGAAAAGGAGCAGGTAT 602
 Db 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAAGTCCAGAAAAGGAGCAGGTAT 600

Qy 603 TCCRTTGCTGTTGACTGGTGTCCCTGGAGTGACGGCATATGAACCTGCTGAGGGCGG 662
 Db 601 TCCRTTGCTGTTGACTGGTGTCCCTGGAGTGACGGCATATGAACCTGCTGAGGGCGG 660

Qy 663 AGACCGTATCATATTGCTCAGTACTCCAGCAAGGAATTGTACACAGCTTGGAGAC 722
 Db 661 AGACCGTATCATATTGCTCAGTACTCCAGCAAGGAATTGTACACAGCTTGGAGAC 720

Qy 723 ACTGTGTAACCTACCTTCTGCTGGTCACTTAAAGCTA 782
 Db 721 ACTGTGTAACCTACCTTCTGCTGGTCACTTAAAGCTA 780

Qy 783 CTCGAACCTAATCCAGACCAAGGATTCTCAAGGAACTTCCCGTAT 842
 Db 781 CTCGAACCTAATCCAGACCAAGGATTCTCAAGGAACTTCCCGTAT 840

Qy 963 AACCCCTCATAGAGAAAAAGGAAAGGATGAGGAAATGAGGAAATTCG 1022
 Db 961 AACCTCTACATAGAAAAAGGAAAGGATGAGGAAATTCG 1020

Qy 1023 GATTCTCTCAGACATGTCTTCAAGAGGCACCTGACTCTGTCAGAAGGAGTTCTATA 1082
 Db 1021 GATTCTCTCAGACATGTCTTCAAGAGGCACCTGACTCTGTCAGAAGGAGTTCTATA 1080

Qy 1083 ATTTCACAGAGAAAGTAAACAGGACTTTAACAAAAGACAACCAAATCTAGCCTTG 1142
 Db 1081 ATTTCACAGAGAAAGTAAACAGGACTTTAACAAAAGACAACCAAATCTAGCCTTG 1140

Qy 1143 GAACAAACCAAGAACCCACAAGTGTGAGGTCTGAGATAACA 1185
 Db 1141 GAACAAACCAAGAACCCACAAGTGTGACAAATGGACA 1183

Qy 1143 GAACAAACCAAGAACCCACAAGTGTGAGGTCTGAGATAACA 1185
 Db 1141 GAACAAACCAAGAACCCACAAGTGTGACAAATGGACA 1183

Qy 123 CAGAAGAATGATAACCAAGAAGATGTGCCAACATGAACTACATGATAAACAAAGTGGCTG 182
 Db 121 CAGAAGAATGATAACCAAGAAGATGTACGAAAGTACATGATAAACAAAGTGGCTG 180

Qy 183 GAGGGCAATGAAAGTGTGAGGAATGTCCTCAAGGAAACTCCAGATCATGCAGGGCTCTGGAGCAC 242
 Db 181 GAGGGCAATGAAAGTGTGAGGAATGTCCTCAAGGAAACTCCAGATCATGCAGGGCTCTGGAGCAC 240

Qy 243 CCTTTCTGGTTAATTGTGTGATTCCCTTCAAGGAACTTCCCGTAT 802

121 CAGAAGGAAATGCCAACGAAAGATGTACGGCAATGGAAGTACATGAAATAACAAAGAAATGCGCTG 180
 Db 241 CCTTTCCCTGGTTAATTGGTGGTATTCTGGGTTACCTGCAAGATGAGAACATGTTCATGGTGGTG 300
 Qy 3 03 GACCTCTGGCTGGAGACCTGGTATTCAACCTGCAACAGAACGTCACCTCAAGGAA 362
 Db 3 01 GACCTCTGGTGGAGACCTGGTATTCAACCTGCAACAGAACGTCACCTCAAGGAA 360
 Qy 3 63 GAAACAGTGAAGGCTTCATCTGTGAGCTGGCATGGGACTACCTGCAGAACCG 422
 Db 3 61 GAAACAGTGAAGGCTTCATCTGTGAGCTGGCATGGCCTGAGAACCG 420
 Qy 3 03 CGCATCATTCACAGGGATATGAAAGCCTGACAATATTCTACTTGACGGAGACCTGGGACTTCAAGGAA 362
 Db 3 01 GACCTCTGGTGGAGACCTGGTATTCAACCTGCAACAGAACGTCACCTCAAGGAA 360
 Qy 3 63 GAAACAGTGAAGGCTTCATCTGTGAGCTGGCATGGGACTACCTGCAGAACCG 422
 Db 3 61 GAAACAGTGAAGGCTTCATCTGTGAGCTGGCATGGGACTACCTGCAGAACCG 420
 Qy 3 03 GACCTCTGGTGGAGACCTGGGACTTCAAGGAAACGTCACCTCAAGGAA 362
 Db 3 01 GACCTCTGGTGGAGACCTGGTATTCAACCTGCAACAGAACGTCACCTCAAGGAA 360
 Qy 3 63 GAAACAGTGAAGGCTTCATCTGTGAGCTGGCATGGGACTACCTGCAGAACCG 422
 Db 3 61 GAAACAGTGAAGGCTTCATCTGTGAGCTGGCATGGGACTACCTGCAGAACCG 420
 Qy 4 23 CGCATCATTCACAGGGATATGAAAGCCTGACAATATTCTACTTGACGGAGACCTGGGACTTCAAGGAA 362
 Db 4 21 CGCATCATTCACAGGGATATGAAAGCCTGACAATATTCTACTTGACGGAGACCTGGGACTTCAAGGAA 360
 Qy 4 83 CACATCACAGATTCAACATTGCTGGGATGCTGGGAGACACAGATTACCCATG 542
 Db 4 81 CACATCACAGATTCAACATTGCTGGGAGACACAGATTACCCATG 540
 Qy 5 43 GCTGGCACCAAGCCTTACATGGGACCTGAGCTCAGGTCAAAGGAGGAGCTAT 602
 Db 5 41 GCTGGCACCAAGCCTTACATGGGACCTGAGGTCAAAGGAGGAGCTAT 600
 Qy 6 03 TCCTTTGCTGACTGGTGGGAGTGAACCTGAGCTGAGGAGCTGAGGCTAT 662
 Db 6 01 TCCTTTGCTGACTGGTGGGAGTGAACCTGAGGCTATGAGACTGCTGAGGCGGG 660
 Qy 6 63 A 663
 Db 6 61 A 661

 RESULT 7
 US-09-841-683-4
 ; Sequence 4, Application US/09841683
 ; Patent No. 6617147
 ; GENERAL INFORMATION:
 ; APPLICANT: Hu, Yi
 ; APPLICANT: Nepomnichy, Boris
 ; APPLICANT: Wang, Xiaoming
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Scoville, John
 ; APPLICANT: Walké, D. Wade
 ; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
 ; FILE REFERENCE: LEX-0167-USA
 ; CURRENT APPLICATION NUMBER: US/09/841,683
 ; CURRENT FILING DATE: 2001-04-24
 ; PRIOR APPLICATION NUMBER: US 60/199,499
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: US 60/201,227
 ; PRIOR FILING DATE: 2000-05-01
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 678
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ;
 US-09-841-683-4
 Query Match 44.1%; Score 655.2; DB 4; Length 678;
 Best Local Similarity 99.5%; Pred. No. 7e-197;
 Matches 657; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 3 ATGGGAGCGAACACTTCAAGAAAACCACCAAGTGTGATGAAAATGAAAGATGTCAACTTT 62
 1 ATGGGAGGCCAACACTTCAAGAAAACCACCAAGTGTGATGAAAATGAAAGATGTCAACTTT 60
 Qy 63 GACCACTTGAATTGGCAAGCCATTGGGAAGGCAAGTGTGATGAAAATGAAAGATGTCAACTTT 62
 61 GACCACTTGAATTGGCAAGCCATTGGGAAGGCAAGTGTGATGAAAATGAAAGATGTCAACTTT 60
 Qy 123 CAGAAGAATGATAACGAAAGATGTGGCAATGAAACTGAAATAACAAAAGTGGCTG 182
 Db 150 GCAATGAACTGAAATAACAAAAGTGGCTGGGAGCGCAATGAAATGAGAAATGCTCTC 209
 Qy

|| APPLICANT: Meyers, Rachel
 || APPLICANT: Kapeller-Liberman, Rosana
 || TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
 || FILE REFERENCE: 35800/209996
 || CURRENT APPLICATION NUMBER: US/09/799, 875
 || CURRENT FILING DATE: 2001-03-06
 || PRIOR APPLICATION NUMBER: 60/182, 059
 || PRIOR FILING DATE: 2000-02-11
 || PRIOR APPLICATION NUMBER: 09/659, 287
 || PRIOR FILING DATE: 2000-09-12
 || NUMBER OF SEQ ID NOS: 32
 || SOFTWARE: FastSEQ for Windows Version 4.0
 || SEQ ID NO 13
 || LENGTH: 1826
 || TYPE: DNA
 || ORGANISM: Homo sapiens
 || FEATURE:
 || NAME/KEY: CDS
 || LOCATION: (17) . . . (1273)
 || US-09-799-875-13

Query Match 32.4%; Score 481.6; DB 4;
 Best Local Similarity 66.5%; Pred. No. 1.2e-141;
 Matches 726; Conservative 0; Mismatches 354; Indels 12; Gaps 2;

Qy 30 CCAGTGTGATGAAAATGAAAGATGTCAACTTGACCACTTGCTGGAGGCCATT 89
 Db 53 CCGGTGTTGACGACAAGGAGGACGTGAACATCCACAGAGATGTCAAGGCCT 112

Qy 90 GGGAAAGGCAGTTGGGGAGGTCCTGCAAGAAGGAATGATAACCAAGAAGATGTGC 149
 Db 113 GGGAAAGGGCAGTTGGCAAGGGAGGACATGTGCAACACTGACCCGACTTCACATGGCCACC 516

Qy 150 GCAATGAAGTACATGAATAAACAAAAGTGGCTGGAGGGCAATGAAGGTGAGAAATGTCTTC 209
 Db 173 GCCATGAAGTACATGAACAAAGCAGGAGGACATGGCTGGCATCTGGTACTTC 232

Qy 210 AGGAACACTCCAGATCATGGAGGGCATGTTCTGGAGGACCCCTTCCTGGTTAATTGTGGTTATTTC 269
 Db 233 CGGGAGGTGGAGATCCTGGAGGACATGTTCTGGTACTGGCAACCTCTGGTACTTC 292

Qy 270 TTCCAAGATGAGGAGACATGTTCTGGAGGACCCCTTCCTGGAGGACCTGGCTGGGT 329
 Db 293 TTCCAGGGAGGAGGACATGTTCTGGTACTGGCAACCTCTGGTACTTC 352

Qy 330 TATCACCTGCAACAGAACGTTCAACTTCAGGAAGAAACAGTGAAGGCTCTCATCTGTGAG 389
 Db 353 TACCCACTGCAAGAACGTTCACTGGTACTGGTACTTC 412

Qy 390 CTGGTCTGGCCCTGGACTACCTGGCAACCCGGCATATGAAGGCT 449
 Db 413 ATGGCACTGGCTCTGGACTACCTGGCAACCCGGCATATGTGAGGAG 472

Qy 510 GACAATATTTACTTGACGAAACATGGCAACATCACAGATTCAACATTGTGAGCTGGCG 509
 Db 473 GACAACATTCTCCACTCTGGATGAGGAGCATGGCACACATGGCACACCTGACCGACTTC 532

Qy 570 GAGATGTTCAAGCTC-----CAGAAAAGGAGGAGGCTTACATGGCACCT 569
 Db 593 GAGATCTCCACTCTGGCTATGAGCTGGGACTGGCTACATGGCTCC 652

Qy 624 TCCCTGGGAGTGACGGCATATGAAGGGCGGACTGCTGAGAGGGCGGACTATTCGCTCC 683
 Db 653 TCGGTGGGGTGTGGCTATGAGCTGGGACTGGCTACATGGCCACT 712

Qy 684 AGTACTTCCAGCAAGGAATTTGTACACACGTTGAGACGACTGGTAACTTACCCCTCT 743

RESULT 9
 US-09-799-875-13
 ; Sequence 13, Application US/097999875
 ; Patent No. 6638721
 ; GENERAL INFORMATION:

Db 713 AGCAACGGCGTGGAGTCCTGGTCAAGGTGACTTAAAGCTACTCTAACCTTAATCGAACCCAA 772
 Qy 744 GCCTGGTCAAGGAATGGTGTCACTCTTAAAGCTACTCTAACCTTAATCGAACCCAA 803
 Db 773 ACGGGGTCAAGGAGATGGTGGCTTGGCTTGGGAGCTGGTGGGAGCTGGCAGCTGGCAC 832
 Qy 804 CGATTTCAGTTAGTTGCAACTTCCCCTATATGAATGATAAATGGGAT 863
 Db 833 CGGCCTCCAGCTCCAGGACGGTGGAGGGCTGGCTGGGAC 892
 Qy 864 GCAGTTTCAGAAGAGGCTCATTCAGGTTCAATTCTAACCTGTAATTGTT 923
 Db 893 CACCTGAGGAGAAGAGGGTGGAGGGCTTGGGCCAACAAAGGCCGCTGCAC 952
 Qy 924 GATCCTACCCCTGAAATGGAAATGGTCCAAACCTCTAACATAAGAAAAAA 983
 Db 953 GACCCCACCTTGAGGAGATGATCCTGGAGTCCAGGGCACAAAGAAGAG 1012
 Qy 984 AAGGGTCTGGCAAAGAAGGA-----GAAGGATATGAGGAATGGGATTCAGACA 1037
 Db 1013 AAGGGTCTGGCCAAGAACAAAGTCCGGACAAACGAGGGACAGCTCCAGTCGAGAAT 1072
 Qy 1038 TGTCCTCTCAAGGACCCTTGACTCTGTCAGAAGGGTTCAACAGAGGA 1097
 Db 1073 GACTATCTCAAGACTGCCATCGATGCATCCAGAACAGACTTCGTGATT 1132
 Qy 1098 AAAGTAAACAGG 1109
 Db 1133 AAGCTGAAGAGGG 1144

RESULT 10
 US-09-819-607-1
 ; Sequence 1, Application US/09819607
 ; Patent No. 6686176
 ; GENERAL INFORMATION:
 ; APPLICANT: BEASLEY, Ellen et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL001078
 ; CURRENT APPLICATION NUMBER: US/09/819, 607
 ; CURRENT FILING DATE: 2001-03-29
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1864
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-819-607-1

Query Match 31.4%; Score 466.8; DB 4; Length 1864;
 Best Local Similarity 65.9%; Pred. No. 5.9e-137;
 Matches 713; Conservative 0; Mismatches 357; Indels 12; Gaps 2;

Qy 40 ATGAAAATGAAATGTTGACCACTTGACCAATTGAAATGATAACCAAGAAGATGGCAATTGGAAAGGCA 99
 Db 89 AAGCAGAGAAGGCAGTGAACCTCGACCACTCCAGATCCTGGGCCATTGGAAAGGGCA 148

Qy 100 GTTTGGGAGGTCTGCAATTGAAATGATAACCAAGAAGATGGCAATTGGAAAGGCA 159
 Db 149 GCTTGGCAAGGTGTGCAACTTGACCACTCCAGATCCTGGGCCATTGGAAAGGGCA 208

Qy 160 ACATGAATAAACAAAATGGGAGGTCTGCAATTGAAATGATAACCAAGAAGATGGCAATTGGAAAGGCA 219
 Db 209 ACATGAATAAACAAAATGGGAGGTCTGCAATTGAAATGATAACCAAGAAGATGGCAATTGGAAAGGGCA 268

Qy 220 AGATCATGCAAGGGTCTGGAGCACCCCTTCCGGTATTCTGGTCAAGGATGCTTCAGGAACCTCCAGGAGT 279
 Db 269 AGATCTGCAAGGAGATCGAGCACTGGTCAACCTCTGGTACTCTGGTCAACCTCCAGGAGC 328

Qy 280 AGGAAGACATGTTCATGGTGGGACCTCCRGCTGGGACCTCCRGCTGGGACCTGGTCAAGGACCTGGTTACACCTRG 339

Db 329 AGGAGGACATGTTCATGGTGGGACCTGGCTTACACCTGGGGACCTGGCTTACACCTGG 388
 Qy 340 AACAGAACGTCCACCTCAAGGAAACAGTGAAGGCTCTCATCTGTGAGGTGGTCACTGG 399
 Db 389 AGCAGAACGTGCAATTCTCCGGACACGGTGGGAGATGGCACTCTGGGACTGG 448
 Qy 400 CCTGGACTACCTGCAAGAACCGGCAATGCACTATTCAAGGGATATGAAGGCTGACAATATT 459
 Db 449 CTCTGGACTACCTGCGGGCCAGCACATCATCCAGAGATGTCAGAACATTC 508
 Qy 460 TACCTGACGAACATGGGACATCACAGATTCAACATGCTGCACTGGCACCTGCTGCCCA 519
 Db 509 TCCTGGATGAGGAGCATGACACCTGACCGACTCAACATGCCACCATCATCAAGG 568
 Qy 520 GGGAGAACACAGATTACCCATGGCAGCTGGCACCTAACATGGCACCTGAGATGGTCA 579
 Db 569 ACGGGGAGGGGAGGGCATAGCAGGGCACAAAGCCGTAATGGCTCCGGAGATCTTCC 628
 Qy 580 GCTC-----CAGAAAGGACAGGCTTAATTCCTGGGAGGGCTTCCCTGGGAG 633
 Db 629 ACTCTTTGTCACCGGGGACTCTCCGGCTACTCCCTGAGGGTAGCTGGTGGGACT 688
 Qy 634 TGACGGCATATGAACTGGCTGAGGCTTAATTCCTGGGAGGGCTTCCAGTCTCA 693
 Db 689 TGATGGCTATGAGCTGTCAGGATGGGGCCTATGACATCCACTCCAGGAACGCG 748
 Qy 694 GCAAGGAAATTGTAACACGTTGAGGACTGTGTAACCTACCCCTCTGCTGGTCA 753
 Db 749 TGGAGTCCTGGTCAACGGTCCAGTGTGTCAGCAACGGTCCAGTGTCCCAC 808
 Qy 754 AGGAATGGTGTCACTCTTAAAGCTACTCGAACCTAACCTGAAACGAAACGGATTTCCTC 813
 Db 809 AGGAGATGGCCCTGTCAGCTCCACTGTGAACCCGAGCCTGGCTCTCCA 868
 Qy 814 AGTTATCTGATGTCAGACTTCCCGTATATGAAATGATAAACCTGGGATGCGAGTTTC 873
 Db 869 GCCTCCAGGAGCTGCGGGCGCCGGGGCTGGCTGGTCACTGGGAGCACCTGG 928
 Qy 874 AGAAGGGCTCATTCAGGTTCATTCCTTAATAAAGGCAGGGCTGAATTGTGATCCTACCT 933
 Db 929 AGAAGGGGGAGCCGGCTTCGTGGCCCAACAAAGGGGACTGGCTGCACTGGACCCACCT 988
 Qy 934 TTGAACCTGGGAAATGATTGGACTCCAAACCTCTACATAAGAAAAAAAGGCTCTGG 993
 Db 989 TTGAGCTGGAGGAGATGTCCTGGACTCCAGCTCCAGGACAGCTCCAGGAAATGACTATCTTC 1047
 Qy 994 CAAAGAAGGA-----GAAGGATATGAGGAATGGCAATTCTCAGACATGGTCTTC 1047
 Db 1049 CCAAGAACAAAGTCCGGGACAACAGGGAGACAGCTCCAGGAACTGGCTGAAATGACTATCTTC 1108
 Qy 1048 AAGAGCACCTGACTCTGTCCAGAAGGGACTTCAACAGAGAAAGTAAACA 1107
 Db 1109 AAGACTGCCTCGATGCCATCCAGCAAGGAAAGCTGAAAGA 1168
 Qy 1108 GG 1109
 Db 1109 GG 1109

RESULT 11
 US-09-801-876B-3
 ; Sequence 3, Application US/09801876B
 ; Patent No. 6492155
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE REFERENCE: CL001160
 ; CURRENT APPLICATION NUMBER: US/09/801, 876B
 ; CURRENT FILING DATE: 2001-03-09
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3 LENGTH: 148567
; TYPE: DNA
; ORGANISM: Human
; FEATURE: misc_feature
; LOCATION: (1) ..(148567)
; OTHER INFORMATION: n = A,T,C or G
US-09-801-876B-3

Query Match Score 363.4; DB 4; Length 148567;
Best Local Similarity 98.4%; Pred. No. 7.6e-103;
Matches 367; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1097 AAAAGTAAACAGGGACTTAAACAAAGACAACCAATCTAGCCTTGGAAACAAACCAAAGA 1156
Db 146198 AAGAGTAAACAGGGACTTAAACAAAGACAACCAATCTAGCCTTGGAAACAAACCAAAGA 146257

Qy 1157 CCCACAAAGGTGAGGGATGGTCAGAATAACAAACFTGTAAGGCCCTCATGTCTTCTTCTGGG 1216
Db 146258 CCCACAAAGGTGAGGGATGGTCAGAATAACAAACCAATCTAGCCTTGGAAACAAACCAAAGA 146317

Qy 1217 ACAATCTCATGCAGAAAACCTCTAAATTACATATGTCAAGAAAAGCTGACAGTAGCTCCCG 1276
Db 146318 ACAATCTCATGCAGAAAACCTCTAAATTACATATGTCAAGAAAAGCTGACAGTAGTTCTTG 146377

Qy 1277 CCACTCCACACCATGACTTAGAAAAATTGTGAATGAAATTCTAAAAAGGCCACCA 1336
Db 146378 CCACTCCACACCATGACTTAGAAAAATTGTGAATGAAATTCTAAAAAGGCCACCA 146437

Qy 1337 ACACAGTGAAGGGTCCGGCCTGAGCTCCTGGAAAGTCATTCCACATCAACTCTGTG 1396
Db 146438 ACACAGTGAAGGGTCCGGCCTGAGCTCCTGGATGTCATTCCACATCAACTCTGTG 146497

Qy 1397 TGATCTAGAGCAAGTCACTTCTGTGTTACTTTATCTAAATGAGA 1456
Db 146498 TGATCTAGAGCAAGTCACTTCTGTGTTACTTTATCTAAATGAGA 146557

Qy 1457 GGTTATACTAAA 1469
Db 146558 GGTTATACTAAA 146570

RESULT 13 US-09-394-455-3
; Sequence 3, Application US/09394455
; Patent No. 6531305
; GENERAL INFORMATION:
; APPLICANT: Witman, George F.
; APPLICANT: San Agustin, Jovenal
; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE
; FILE REFERENCE: 07917/078001
; CURRENT APPLICATION NUMBER: US/09/394,455
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/099,771
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ For Windows Version 4.0
; SEQ ID NO 3 LENGTH: 1008
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) . . . (1008)
; US-09-394-455-3

Query Match Score 132.6; DB 4; Length 1008;
Best Local Similarity 54.1%; Pred. No. 2e-31;
Matches 323; Conservative 0; Mismatches 259; Indels 15; Gaps 2;

Qy 54 GTCAACTTGCACACTTGAATTTGGGAGCCATTGGGAAAGGCAGTTGGGAGGCTC 113
Db 70 GCCCACTGGATCAGTTGAACGAATCAAGACCCCTGGCACGGGCTCGGGGGTGTG 129

Qy 114 TGCATTGTCAGAGAATGATAACCAAGAATGTGCGCAATGAAGTACATGAATAACCAA 173
Db 130 ATGCTGGTGAACACAGATCGAACACAGAGCCACTATGCCATGAAGATCCTCGAACAG 189

Qy 174 AAGTGGCTGGAGGCAATGAAGTGAAGAATGTCTTCAAGGAACCTCCAGATCATGGAGGT 233
Db 190 AAGGGTGGTGAACACAGATCGAACACAGAGCCACTATGCCATGAAGATCCTCGAACAG 249

Query Match Score 363.4; DB 4; Length 148567;
Best Local Similarity 98.4%; Pred. No. 7.6e-103;
Matches 367; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 234 CTGGAGCACCCCTTCTGGTTAATTGTGTATTCCCTCCAAGTGAAGAACATGTGTC 293
Db 250 GTCAACTTCCGTTCTCGTCAAACTCGAGTTCTCCCTCAAGGACAACCTAACTTAC 309

Qy 1097 AAAAGTAAACAGGGACTTAAACAAAGACAACCAATCTAGCCTTGGAAACAAACCAAAGA 1156

294 ATGGTGTGGACCTCCTGGAGACCTGGTGTATCACCTGCAACAGAACGTCAC 353
 310 ATGGTCATGGAGTACGTGGCCGGAGATGTTCTCACACCTACGGGGATGGAGG 369

QY 354 TICAGGAAGAACAGTGAAGGCTCTCATCTGTGAGCTGGTCATGGCCCTGGACTACCTG 413
 370 TTCACTGAGGCCATGGCGTTCTACGGGGCCAGATCGTCCCTGACCTTGAGTATCTG 429

Db 414 CAGAACCCAGGGCATCATTCAACAGGATATGGACATATTTCAGGATATTTCAGGAAACAT 473
 555 CACTCGCTGGATCTCATCTACAGGGACTGAGCTGAAGCCGGAGAATCTGCTCATTGAGCAG 614

QY 474 GGGCACCTGGCACATCACAGATTCAACATTGCTGGATGGTGCCTGCCAGGGAGACACAGATT 533
 615 GGCTACATTCAAGTGACAGACTTCGTTTGCCAA----GGCGTGAAGGGCGGCACT 668

Db 474 GGGCACCTGGCACATCACAGATTCAACATTGCTGGATGGTGCCTGCCAGGGAGACACAGATT 533
 615 GGCTACATTCAAGTGACAGACTTCGTTTGCCAA----GGCGTGAAGGGCGGCACT 668

QY 534 ACCACCATGGCTGGCACCAAGGCCTTACATGGCACCTGAGATGGTCAAGTGGAAACAGA 593
 669 TGGACCTTGTGGGCCACCCCTGAGTACTGGCCCTGAGATTATCCTGAGCAA---- 721

Db 534 ACCACCATGGCTGGCACCAAGGCCTTACATGGCACCTGAGATGGTCAAGTGGAAACAGA 593
 669 TGGACCTTGTGGGCCACCCCTGAGTACTGGCCCTGAGATTATCCTGAGCAA---- 721

QY 474 GGGCACCTGGCACATCACAGATTCAACATTGCTGGATGGTGCCTGCCAGGGAGACACAGATT 533
 490 GGCTACATTCAAGTGACAGACTTCGTTTGCCAA----GGCGTGAAGGGCGGCACT 543

Db 534 ACCACCATGGCTGGCACCAAGGCCTTACATGGCACCTGAGATGGTCAAGTGGAAACAGA 593
 722 -AGGCTACAACAAGGCCGTGGACTGGTGGCCCTGGGGCTTCTGGGGACTGGTGGAAATG 776

Db 544 TGGACCTTGTGGGCCACCCCTGAGTACTGGCCCTGAGATTATCCTGAGCAA---- 596

QY 594 GCAGGCTATTCCCTGGTGTGACTGGTGGCCTTGGGAGTGACGGCATATGAACTG 650
 597 -AGGCTACAACAAGGCCGTGGACTGGGGCTGGGTTCTATCTATGAAATG 651

Db 594 GCAGGCTATTCCCTGGTGTGACTGGTGGCCTTGGGAGTGACGGCATATGAACTG 650
 597 -AGGCTACAACAAGGCCGTGGACTGGGGCTGGGTTCTATCTATGAAATG 651

RESULT 15
 US-09-394-455-5
 ; Sequence 5, Application US/09394455
 ; Patent No. 6531305

; GENERAL INFORMATION:
 ; APPLICANT: Witman, George F.
 ; APPLICANT: San Agustin, Jovenal
 ; APPLICANT: Leszyk, John D.
 ; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASES, CORRESPONDING
 ; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASES, CORRESPONDING
 ; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASES, CORRESPONDING
 ; FILE REFERENCE: 07917/078001
 ; CURRENT APPLICATION NUMBER: US/09/394,455
 ; CURRENT FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: US 60/099,771
 ; PRIOR FILING DATE: 1998-09-10
 ; NUMBER OF SEQ ID NOS: 56
 ; SEQ ID NO: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 5
 ; LENGTH: 2549
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (81) .. (1136)
 ; NAME/KEY: unsure
 ; LOCATION: 6
 ; OTHER INFORMATION: unknown
 ; US-09-467-082-3

QY 54 GTCAACTTGCACCACTTGAATTTGGGAGCCATTGGGAAAGGCAGTTTGGGGAGGTC 113
 195 GCCCACTTGGATCAGTTGAACGAATCAAGACCCCTGGCACGGCTCCTCGGGGGGTG 254

Db 114 TGCATTGTACAGAAGAATGATAACCAAGAAGATGTGGCAATGAAAGTACATGAAATAACAA 173
 255 ATGCTGGTGAACACAGGAGACGGGAACCACTATGCCATGAAGATCCTCGACAAACAG 314

QY 174 AAGTGGTGGAGGCAATGAGAATGAGATGGAAATGTGGCAATGAAAGTACATGCAAGGTT 233
 315 AAGTGGTGAACACAGGAGACGGGAACCACTATGCCATGAAGATCCTCGACAAACAG 314

Db 234 CTGGAGCACCCCTTCCGGTAAATTGGTGTATTCCTTCCAAAGATGAGGAAGACATGTTG 293
 375 GTCAACTTCCGGTCCCTCGTCAACTCGAGTTCTCCCTCAAGGACAACACTAACTATAAC 434

QY 294 ATGGTGGTGGAGCCTCCCTGGAGACCTGGTATCACCTGCAACAGAACGTCAC 353
 435 ATGGTCATGGAGTAGTACGGTGGCCGGGGAGATGGTTCTCACACCTACGGGGATCGGAAGG 494

Db 354 TTCAAGGAAGAACAGTGAAGGCTCTTCAATCTGTGAGCTGGTCAATGGCCCTGGACTACCTG 413

Qy	354	TTCAGGAAACAGTGAAGCTCTTCAATCTGTGAGCTGGTCAATGGCCCTGGACTACCTG	413
Db	495	TTCAGTGAGCCCCATGCCCGTTCTACGGGCCAGATCGTCCCTGACCTTGAGTATCTG	554
Qy	414	CAGAACCAGCGCATCATTCAACAGGGATATGAAGCTGACAATATTTTACCTGACGAACAT	473
Db	555	CACTCGCTGGATCTCATCTACAGGGACCTGAAGCCGGAGAAATCTGCTCATTGACCCAGCAG	614
Qy	474	GGGCACGTGCACATCACAGATTCAACATTGCTGGATGCTGCCAGGGAGACACAGATT	533
Db	615	GGCTACATTCAAGTGACAGACTCGGTTGCCAA-----GGCGGTGAAGGGCCGCACT	668
Qy	534	ACCAACCATTGGCTGGCCAAGCCTTACATGGCACCTGAGATGTTCAGCTCCAGAAAAAGGA	593
Db	669	TGGACCTTGTGGGCCACCCCTGAGTACCTGGCCCTGAGATTCTGAGATTCCTGAGCAA-----	721
Qy	594	GCAGGGCTATTCCCTTGTGACTGGTGGCTGGAGGTGACGGCATATGAACTG	650
Db	722	-AGGCTACAAACAAAGCCGGACTGTTGGGGCTGGGGTTCTATCTATGAAATG	776

Search completed: June 26, 2004, 23:09:37
Job time : 99 secs

PS Claim 4; Fig 1; 174pp; English.

The present invention relates to the isolation of a human kinase and the polynucleotide sequences encoding it. The human kinase of the invention is related to the serine/threonine kinase subfamily. The gene encoding the human kinase is located on chromosome 5. The polypeptide and polynucleotide sequences of the invention are useful for treating a disease or condition mediated by a human kinase. Both the polypeptide and polynucleotide sequences are useful as models for the development of human therapeutics, for identifying therapeutic proteins, as targets for development of human therapeutic agents, and as query sequences to perform a search against sequence data bases to identify other family members of related sequences. The polypeptide is useful to raise antibodies or to elicit another immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as markers for tissues in which the corresponding protein is preferentially expressed, in drug screening assays, in cell-based or cell-free systems, to identify compounds that modulate kinase activity of the protein in its natural state, or an altered form that causes the specific disease or pathology associated with the kinase, to screen a compound for the ability to stimulate or inhibit interaction between the kinase protein and a molecule that normally interacts with the kinase protein, and in pharmacogenomic analysis. The polynucleotide is useful for monitoring the effectiveness of modulating compounds on the expression or activity of the human kinase gene in clinical trials or in a treatment regimen, in diagnostic assays for qualitative changes in a human kinase nucleic acid that leads to a pathology, for testing an individual for a genotype that while not necessarily causing a disease, nevertheless affects the treatment modality, as antisense constructs to control human kinase gene expression in cells, tissues and organisms, for gene therapy in patients containing cells that are aberrant in human kinase gene expression, and to produce transgenic animals. The present sequence encodes a human kinase related to the serine/threonine protein kinase subfamily.

SQ Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;

Query Match 100.0%; Score 1485; DB 7; Length 1485;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCATGGGAGAACACTTCAGAAACCCAGTGTGATGAAATGAAGATGTCACT 60	DB	1081	TAATTTCACAGAGAAAAGTAACAAAAGACAACCAAATCTAGCT 1140
DB	1	CCATGGGAGAACACTTCAGAAACCCAGTGTGATGAAATGAAGATGTCACT 60	DB	1081	TAATTTCACAGAGAAAAGTAACAAAAGACAACCAAATCTAGCT 1140
QY	61	TTGACCACATTGAAATTTCGGAGCCATTGGMAAGGCAGTTGGGGAGGTCTGATTG 120	DB	1141	TGAAACAACCAAGGCCAACAGGTGAGGTGGTCAAAATAACAAACTTGTAAAGGCCCTC 1200
DB	61	TTGACCACATTGAAATTTCGGAGCCATTGGGAAGGCATTGGGGAGGTCTGATTG 120	DB	1141	TGAAACAACCAAGGCCAACAGGTGAGGTGGTCAAAATAACAAACTTGTAAAGGCCCTC 1200
QY	121	TACAGAAGAATGATAACCAAGAAGATGTGGCAATGAAGTACATGAATAACAAAGTGCG 180	DB	1201	ATGTCCTCTTCTGGGACAATCTCATGGCAGAAACTCTAAATTACATATGTCAAGAAAAG 1260
DB	121	TACAGAAGAATGATAACCAAGAAGATGTGGCAATGAAGTACATGAATAACAAAGTGCG 180	DB	1261	CTGACAGTAGCTCCCTGGCAACTCCACACCCATGCCACTCCACATGACTTGTGAAATATTT 1320
QY	181	TGGAGGCCAATGAAAGTGAAGAATGTTCAAGGAACCTCCAGATCATGGTGG 240	DB	1261	CTGACAGTAGCTCCCTGGCAACTCCACACCCATGCCACTCCACATGACTTGTGAAATATTT 1320
DB	181	TGGAGGCCAATGAAAGTGAAGAATGTTCAAGGAACATGGTCAAGGAGACATGGTGG 240	DB	1321	CAAAAAAGGGCAGCACACAGTGAAGGGTCTGGGAAGTGTGAAAGTGTGAAATATTT 1380
QY	241	ACCCCTTCCGGTTAATTGGGTATTCCTTCCAAGAATGAGGAAGACATGGTCAAGG 300	DB	1321	CAAAAAAGGGCAGCACACAGTGAAGGGTCTGGGAAGTGTGAAATATTT 1380
DB	241	ACCCCTTCCGGTTAATTGGGTATTCCTTCCAAGAATGAGGAAGACATGGTCAAGG 300	DB	1381	ACATCAATCAACTGTGTGATCTAGCCAGTCACTTGGCCACTTTCTGTGCTTTACTTTA 1440
QY	301	TGGGACCTCCRGTCGGTGGAGACCTGCGTAACTCTGGTATCATGGTCAAGG 360	DB	1381	ACATCAATCAACTGTGTGATCTAGCCAGTCACTTGGCCACTTTCTGTGCTTTACTTTA 1440
DB	301	TGGGACCTCCRGTCGGTGGAGACCTGCGTAACTCTGGTATCATGGTCAAGG 360	DB	1441	TTTATCTAAATGAGGGTTATACTAaaaaaaaaaaaaaa 1485
QY	361	AAGAAACAGTGAAGCTTCACTCTGAGCTGGACTACCTGGCAAGAACC 420	DB	1441	TTTATCTAAATGAGGGTTATACTAaaaaaaaaaaaaaa 1485
DB	361	AAGAAACAGTGAAGCTTCACTCTGAGCTGGACTACCTGGCAAGAACC 420	DB	1485	RESULT 2 ACA62840 ID ACA62840 standard; cDNA; 1485 BP. XX

AC	ACA62840;	Db	61 TTGACCACTTGAATTTCGGAGCCATTGGAAAGGCAGTTGGGAGGTCTGCATTG 120
XX	01-SEP-2003 (first entry)	Qy	121 TACAGAACATGATACCAAGAAGATGTGCCAATGAAAGTACATGATAAAAGTGGC 180
XX	CDNA encoding human kinase.	Db	121 TACAGAACATGATACCAAGAAGATGTGCCAATGAAAGTACATGATAAAAGTGGC 180
XX	Human; ss; gene; kinase; gene therapy; cancer; inflammation; psoriasis; arteriosclerosis.	Qy	181 TGGAGCGCAATGAAAGTGAGAAATTGTCTCAAGGAACCTCAGATCATGCACTGGAGC 240
KW	KW	Db	181 TGGAGCGCAATGAAAGTGAGAAATTGTCTCAAGGAACCTCAGATCATGCACTGGAGC 240
XX	Homo sapiens.	Qy	241 ACCCTTTCTGGTTAATTGTGTATTCTCCAAGATGAGGAAGACATGTTCATGGTGG 300
OS		Db	241 ACCCTTTCTGGTTAATTGTGTATTCTCCAAGATGAGGAAGACATGTTCATGGTGG 300
XX	Key	Location/Qualifiers	
FH	5' UTR	1 . 2	
FT	CDS	/*tag= a 3 .1193	
FT	PT	/*tag= b /product= "Kinase"	
FT	3' UTR	1194 . 1475	
FT	PT	/*tag= c 361 AAGAAACAGTGAACTGCTTCACTGTGAGCTGGTCACTGGGCTTGAGAAC 420	
XX	US20030227307-A1.	Db	361 AAGAAACAGTGAACTGCTTCACTGTGAGCTGGTCACTGGGCTTGAGAAC 420
XX	PD .FEB-2003.	Qy	421 AGCGCATATTCAAGGGATATGAGCCTGACAATTATTTCAGCTGGCAC 480
XX	26-SEP-2002; 2002US-00254869.	Db	421 AGCGCATATTCAAGGGATATGAGCCTGACAATTATTTCAGCTGGCAC 480
XX	09-MAR-2001; 2001US-00801876.	Qy	481 TGCACATCACAGATTCAACATGCTGCAATGCTGCATGGGAGACAGATTACACCA 540
XX	(APPL-) APPLERA CORP.	Db	481 TGCACATCACAGATTCAACATGCTGCAATGCTGCATGGGAGACAGATTACACCA 540
PI	Ye J, Yan C, Di Francesco V, Beasley EM;	Qy	541 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTAGCTCCAGAAAGGAGGGCT 600
XX	WPI; 2003-492035/58.	Db	541 TGGCTGGCACCAAGCCTTACATGGCACCTGAGATGTTAGCTCCAGAAAGGAGGGCT 600
DR	DR; ABU62276.	Qy	601 ATTCCTTGCTGTTGACTCTGGTCCAGTGGACTGGTGTGCTGTTGACTGGGCTATGAGTGGCTGAGGGCC 660
PT	New isolated human kinase proteins, useful for treating disorders mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis or psoriasis), or for development of human therapeutics and diagnostic compositions.	Db	601 ATTCCTTGCTGTTGACTCTGGTGTGCTGTTGACTGGGCTATGAGTGGCTGAGGGCC 660
PT	XX	Qy	661 GGAGACCGTATCATATTGCTCAGTACTCCAGCAAGGAAATTGTACACAGTTGAGA 720
PA	XX	Db	661 GGAGACCGTATCATATTGCTCAGTACTCCAGCAAGGAAATTGTACACAGTTGAGA 720
PS	Claim 4; Fig 1; 185pp; English.	Qy	721 CGACTGTGTAACTTACCCCTCTGCCATTGAGAAATGGGTCACTTAAAGAC 780
XX	XX	Db	721 CGACTGTGTAACTTACCCCTCTGCCATTGAGAAATGGGTCACTTAAAGAC 780
CC	The invention relates to a new isolated human kinase peptide. The human kinase peptide and nucleic acid molecules are useful in the development of human therapeutics and diagnostic compositions. The peptides are useful for treating disorders (e.g. cancers, inflammations, arteriosclerosis or psoriasis) characterised by an absence of, inappropriate, or unwanted expression of the kinase protein. These molecules are particularly useful as models for developing human therapeutic targets, identifying therapeutic proteins, or serving as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The peptides are also useful for raising antibodies or eliciting an immune response, as a reagent (including the labelled reagent) in assays designed to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids; or as markers for tissues in which the corresponding protein is preferentially expressed. The agents identified are useful for treating a subject with a disorder mediated by kinase pathway. The present sequence represents cDNA encoding a human kinase.	Qy	781 TACTCGAACCTAAATCCAGACCAAGGATTTCAGTTATCTGATGTTCACTTCCGGT 840
CC		Db	781 TACTCGAACCTAAATCCAGACCAAGGATTTCAGTTATCTGATGTTCACTTCCGGT 840
CC		Qy	841 ATATGAATGATATAAAACTTGGGATGCAATTCCAGGTTTCAGAAAGGCTCATTC 900
CC		Db	841 ATATGAATGATATAAACTTGGGATGCAATTCCAGGTTTCAGAAAGGCTCATTC 900
CC		Qy	901 CTAATAAGGCCAGGTGAATTGATCTTGCACGGTTTCAGAAAGGCTCATTC 960
CC		Db	901 CTAATAAGGCCAGGTGAATTGATCTTGCACGGTTTCAGAAAGGCTCATTC 960
CC		Qy	961 CCAAACCTCTACATAGAAAAAAAGGCTCTGGCAAAGGAGGATATGAGGAAT 1020
CC		Db	961 CCAAACCTCTACATAGAAAAAAAGGCTCTGGCAAAGGAGGATATGAGGAAT 1020
SQ	Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;	Qy	1021 GCGATTCTTCTCAGACATGCTCTTCAGAGCACCTGACTCTGTCAGAAGGAGTTCA 1080
	Query Match 100.0%; Score 1495; DB 8; Length 1495;	Db	1021 GCGATTCTTCTCAGACATGCTCTTCAGAGCACCTGACTCTGTCAGAAGGAGTTCA 1080
	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	Qy	1081 TAATTTCAACAGAACAAAAGTAAACAGGAACTTACAAAGAACCAAATCTAGCCT 1140
	Matches 1485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	1081 TAATTTCAACAGAACAAAAGTAAACAGGAACTTACAAAGAACCAAATCTAGCCT 1140
Qy	1 CCATGGGAGGCCAACACTTCAAGAAAACACCAGTGTGTTGATGAAAGATGTCAACT 60	Db	1141 TGGAAACAACCAAGGCCAACACTTCAAGAAAACACCAGTGTGTTGATGAAAGATGTCAACT 60
Db	1 CCATGGGAGGCCAACACTTCAAGAAAACACCAGTGTGTTGATGAAAGATGTCAACT 60	Qy	1141 TGGAAACAACCAAGGCCAACACTTCAAGAAAACACCAGTGTGTTGATGAAAGATGTCAACT 60
Qy	61 TTGACCACTTGAATTTCGGAAAGGCAGTTGGGAGGTCTGCATTG 1200	Db	1141 TGGAAACAACCAAGGCCAACACTTCAAGAAAACACCAGTGTGTTGATGAAAGATGTCAACT 1200

1201	ATGCTCTTCTGGGACAATCTCATGCCAGAAACTCTAATTACATATGTCAGAAAG	1260	lung cancer (claimed), and methods for evaluating the efficacy of treatment. 14911 nucleic acids are useful in diagnostic, screening and gene therapy methods, for recombinant protein production, in the design of probes and primers, as a pharmacogenomics marker, and in the breeding of transgenic animals in which a 14911 gene is introduced or disrupted.
1201	ATGCTCTTCTGGGACAATCTCATGCCAGAAACTCTAATTACATATGTCAGAAAG	1260	Antisense 14911 and ribozyme molecules are used in a claimed method of treating cancer or a cellular proliferation and/or differentiation disorder. In addition to cancer, such disorders include those associated with bone metabolism, autoimmune diseases, cardiovascular disorders, liver disorders, viral diseases, pain and metabolic disorders
1261	CTGACAGTAGCTCCTGCACACTCCACACCATGACTTAGAAAATGTGAATATAATT	1320	XX
1261	CTGACAGTAGCTCCTGCACACTCCACACCATGACTTAGAAAATGTGAATATAATT	1320	SQ Sequence 1281 BP; 392 A; 277 C; 299 G; 313 T; 0 U; 0 Other;
1381	ACATCAATCAACTGTGTGATCTAGGAAAGTCACTTCTGTGCTTTACCTTA	1440	Query Match 82.7%; Score 1228.6; DB 6; Length 1281;
1381	ACATCAATCAACTGTGTGATCTAGGAAAGTCACTTCTGTGCTTTACCTTA	1440	Best Local Similarity 99.7%; Pred. No. 0;
Db	Matches 1231; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		Matches 1231; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	1 CCATGGGAGCGAACACTTCAGAGAAAAGCCATTGGGAGGTCATGCCATTG	120	Qy 1 CCATGGGAGCGAACACTTCAGAGAAAAGCCATTGGGAGGTCATGCCATTG
Db	47 CCATGGGAGGCCAACACTTCAAGAAAACCACAGTGTGAAATGAGTCAACT	106	Db 47 CCATGGGAGGCCAACACTTCAAGAAAACCACAGTGTGAAATGAGTCAACT
Qy	61 TTGACCACTTTGAAATTGGAGGGCAGTTTGAGGGAGGTTCTGGCATTG	120	Qy 61 TTGACCACTTTGAAATTGGAGGGCAGTTTGAGGGAGGTTCTGGCATTG
Db	107 TTGACCACTTTGAAATTGGAGGGAGGTTCTGGCATTG	166	Db 107 TTGACCACTTTGAAATTGGAGGGAGGTTCTGGCATTG
Qy	121 TACAGAAGAATGATAACCAAGAAGATGTCGCAATGAATAAACAAAAGTGGC	180	Qy 121 TACAGAAGAATGATAACCAAGAAGATGTCGCAATGAATAAACAAAAGTGGC
Db	167 TACAGAAGAATGATAACCAAGAAGATGTACGGCAATGAATAAACAAAAGTGGC	226	Db 167 TACAGAAGAATGATAACCAAGAAGATGTACGGCAATGAATAAACAAAAGTGGC
Qy	181 TGGAGGCCAATGAAAGTGGAGAAATGTCTCAAGGAACCTCCAGATCATG	240	Qy 181 TGGAGGCCAATGAAAGTGGAGAAATGTCTCAAGGAACCTCCAGATCATG
Db	227 TGGAGGCCAATGAAAGTGGAGAAATGTCTCAAGGAACCTCCAGATCATG	286	Db 227 TGGAGGCCAATGAAAGTGGAGAAATGTCTCAAGGAACCTCCAGATCATG
Qy	241 ACCCTTTCTGGTTAATTGGGTATTCTTCCAAGATGAGGAACATGTTCATGGT	300	Qy 241 ACCCTTTCTGGTTAATTGGGTATTCTTCCAAGATGAGGAACATGTTCATGGT
Db	287 ACCCTTTCTGGTTAATTGGGTATTCTTCCAAGATGAGGAACATGTTCATGGT	346	Db 287 ACCCTTTCTGGTTAATTGGGTATTCTTCCAAGATGAGGAACATGTTCATGGT
Qy	301 TGGACCTCTGCTGGAGACCTGGTTATCACCTGCAACAGAACGTCACCTCAAGG	360	Qy 301 TGGACCTCTGCTGGAGACCTGGTTATCACCTGCAACAGAACGTCACCTCAAGG
Db	347 TGGACCTCTGCTGGAGACCTGGCTCATCTGCAACAGAACGTCACCTCAAGG	406	Db 347 TGGACCTCTGCTGGAGACCTGGCTCATCTGCAACAGAACGTCACCTCAAGG
Qy	361 AAGAAACAGTGAAGGTCTTCACTCTGAGCTGGACTACCTGAGAACACC	420	Qy 361 AAGAAACAGTGAAGGTCTTCACTCTGAGCTGGACTACCTGAGAACACC
Db	407 AAGAAACAGTGAAGGTCTTCACTCTGAGCTGGACTACCTGAGAACACC	466	Db 407 AAGAAACAGTGAAGGTCTTCACTCTGAGCTGGACTACCTGAGAACACC
Qy	421 AGGGCATCTTCACTGGATATGAAAGCCTGCTGAGCTGGCACC	480	Qy 421 AGGGCATCTTCACTGGATATGAAAGCCTGCTGAGCTGGCACC
Db	467 AGGGCATCTTCACTGGATATGAAAGCCTGCTGAGCTGGCACC	526	Db 467 AGGGCATCTTCACTGGATATGAAAGCCTGCTGAGCTGGCACC
Qy	481 TGCACATCACAGATTCAACATGCTGGGATGCTGCCAGGGAGACACAGATTACCA	540	Qy 481 TGCACATCACAGATTCAACATGCTGGGATGCTGCCAGGGAGACACAGATTACCA
Db	527 TGCACATCACAGATTCAACATGCTGGGATGCTGCCAGGGAGACACAGATTACCA	586	Db 527 TGCACATCACAGATTCAACATGCTGGGATGCTGCCAGGGAGACACAGATTACCA
Qy	541 TGGCTGGGACCAAGCCTTACATGGCACCTGAGATGTTCACTGCTCCAGAAAAGGAGCAGGCT	600	Qy 541 TGGCTGGGACCAAGCCTTACATGGCACCTGAGATGTTCACTGCTCCAGAAAAGGAGCAGGCT
Db	587 TGGCTGGGACCAAGCCTTACATGGCACCTGAGATGTTCACTGCTCCAGAAAAGGAGCAGGCT	646	Db 587 TGGCTGGGACCAAGCCTTACATGGCACCTGAGATGTTCACTGCTCCAGAAAAGGAGCAGGCT
Qy	601 ATTCCCTTGGCTGTTGACTGGTCTCCAGTACTTCCAGGAAGGAAATTGTACACAGTTGAGA	720	Qy 601 ATTCCCTTGGCTGTTGACTGGTCTCCAGTACTTCCAGGAAGGAAATTGTACACAGTTGAGA
Db	707 GGAGACCGTATATTGCTTAACCTACCTTCTGGCTTCAAGGAATATTGTACACAGTTGAGA	766	Db 707 GGAGACCGTATATTGCTTAACCTACCTTCTGGCTTCAAGGAATATTGTACACAGTTGAGA
Qy	721 CGACTGTGTTGTAACCTACCCCTCTGGCTGTCAGGAAATGGTGTCACTCTTAAAGC	780	The present cDNA sequence, the coding region of which is also claimed, encodes a novel human protein kinase, designated 14911 (see AAM50334).
Db	767 CGACTGTGTTGTAACCTACCCCTCTGGCTGTCAGGAAATGGTGTCACTCTTAAAGC	826	This protein kinase plays a role in, or functions in, the transduction of signals for cell proliferation, differentiation and apoptosis, modulating the activity of one or more proteins involved in cellular growth or differentiation. 14911 molecules are overexpressed in some tumour cells, where they may inappropriately propagate either cell proliferation or cell survival signals. The invention provides methods for the diagnosis and treatment of cancer, including breast colon, brain and especially
Qy	781 TACTCGAACCTAACTCCAGAACCAACGATTCTGAGTTATCTGATGTCCAGAACACTTCCCGT	840	Claim 1 (a); Fig 1A-B; 115pp; English.
Db	827 TACTCGAACCTAACTCCAGAACCAACGATTCTGAGTTATCTGATGTCCAGAACACTTCCCGT	886	Novel protein kinase nucleic acid molecules and the encoded proteins for diagnosing and treating cellular proliferative, bone, immune, cardiovascular, liver, pain or metabolic disorders and identifying modulators.

QY	841	ATATGAATGATATAAACTGGGATGCCAGTTTTCAGAAGAGGGCTCATTCCAGGTTCATTC	900
Db	887	ATATGAATGATATAAACTGGGATGCCAGTTTTCAGAAGAGGGCTCATTCCAGGTTCATTC	946
QY	901	CTAATAAGGCAGGCTGAATTGTGATCCTACCTTGAACCTTGAGGAATGATTGGAGT	960
Db	947	CTAATAAGGCAGGCTGAATTGTGATCCTACCTTGAACCTTGAGGAATGATTGGAGT	1006
Qy	961	CCAAACCTCTACATAAGAAAAAAAGCCGTCTGGCAAAGAAGGGATAATGAGGAAT	1020
Db	1007	CCAAACCTCTACATAAGAAAAAAAGCCGTCTGGCAAAGAAGGGATAATGAGGAAT	1066
Qy	1021	GCGATTCTTCTCAGACATGCTCTCAAGGACCTTGACTCTGTCAGGAGTTCA	1080
Db	1067	GCGATTCTTCTCAGACATGCTCTCAAGGACCTTGACTCTGTCAGGAGTTCA	1126
Qy	1081	TAATTTCAACAGAGAAAAAGTAACAGGACTTTAACAAAGACAACCAAATCTAGCCT	1140
Db	1127	TAATTTCAACAGAGAAAAAGTAACAGGACTTTAACAAAGACAACCAAATCTAGCCT	1186
Qy	1141	TGGAAACAAACCAAGGACCCACAAGGTGAGGATGGTCAAGATAACCAACTTGTAAAGGCCTC	1200
Db	1187	TGGAAACAAACCAAGGACCCACAAGGTGAGGATGGTCAAGATAACCAACTTGTAAAGGCCTC	1246
Qy	1201	ATGTCTTCTTGGGACAAATCTCATGCCAGAAC	1235
Db	1247	ATGTCTTCTTGGGACAAATCTCATGCCAGAAC	1281

RESULT 4
AAH46891 AAH46891 standard; cDNA; 1594 BP.
AAH46891;
25-SEP-2001 (first entry)
cDNA encoding human protein kinase SGK177.
Protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human; antiparkinsonian; virucide; antibacterial; antifungal; antimigraine; analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic; antipsoriatic; antirheumatic; antiarthritic; ophthalmological; anorectic; osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic; vasotropics; antidiabetic; gene therapy; ss.
Homo sapiens.

Key CDS
Location/Qualifiers
404. .1594
/*tag= a

WO200155356-A2.

11

02-AUG-2001.

25-JAN-2001: 200

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25-JAN-2000; 2000

31-JAN-2000; 2000

17 = MAB - 2000 ;

29-MAR-2000; 2000;

13-NOV-2000; 2000

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(SUGE-) SUGEN IN

Plowman G. White

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WPI; 2001-476202

P-PSDB; AAB85491

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PT	viral infections, diabetes, obesity, organ transplant rejection and rheumatoid arthritis.
XX	Example 1, Page 201; 218pp; English.
CC	The invention provides human protein kinases and protein kinase-like enzymes and polypeptides encoding the polypeptides. The kinase polypeptides and their modulators are useful for treating a disease or disorder such as cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated disease and metabolic disorders, including cancers of tissues, cancers of hematopoietic origin, diseases of the central nervous system, diseases of the peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, bacteria and fungi, ocular diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypertension, hypertension, psychotic disorders, neurological disorders, dyskinesias, metabolic disorders, and organ transplant rejection. They are also useful for treating rhinitis, autoimmunity, atherosclerosis, psoriasis, osteoarthritis, asthma, chronic inflammatory pelvic disease, chronic inflammatory bowel disease, rheumatoid arthritis, metabolic disorders such as diabetes, obesity, cardiovascular diseases such as reperfusion injury, coronary thrombosis, clotting disorders and atherosclerosis, ocular diseases such as glaucoma, retinopathy and macular degeneration, psychiatric and neurological disorders such as anxiety, schizophrenia, dementia, manic depression, etc. The polymucleotides are useful in gene therapy techniques to treat the above mentioned disorders. Sequences AAH46891-46922 represent human protein kinases encoding cDNA molecules
XX	Sequence 1594 BP; 441 A; 386 C; 395 G; 372 T; 0 U; 0 Other;
QY	Query Match 80.0%; Score 1188.2%; DB 4; Length 1594;
DB	Best Local Similarity 99.7%; Pred. No. 0; Matches 1190; Conservative 0; Mismatches 3; Indels 0; Gaps 0
QY	1 CCATGGGAGCGAACACTTCAAGAAAACCACGCCATTGGAAAGGCAATTGGGAGGTCTGCATTG
DB	402 CCATGGGAGGCCAACACTTCAAGAAAACCACGCCATTGGAAAGGCAATTGGGAGGTCTGCATTG 461
QY	61 TTGACCACTTGAATTTGGAGGCCATTGGAAAGGCAATTGGGAGGTCTGCATTG 120
DB	462 TTGACCACTTGAATTTGGAGGCCATTGGAAAGGCAATTGGGAGGTCTGCATTG 521
QY	121 TACAGAAGAAATGATAACAGAAAGATGTGGCAATGAAGTACATGAATAACAAAAGTGGC 180
DB	522 TACAGAAGAAATGATAACAGAAAGATGTGGCAATGAAGTACATGAATAACAAAAGTGGC 581
QY	181 TGGAGGGCAATGAAGTGAGAAATGTCTTCAGGAAACTCCAGATCATGGGGTCTGGAGC 240
DB	582 TGGAGGGCAATGAAGTGAGAAATGTCTTCAGGAAACTCCAGATCATGGGGTCTGGAGC 641
QY	241 ACCCTTTCTGGTTAATTGGGTATTCCCAAGATGAGGAAGACATGTTCATGGTGG 300
DB	642 ACCCTTTCTGGTTAATTGGGTATTCCCAAGATGAGGAAGACATGTTCATGGTGG 701
QY	301 TGGACACTCTGCTGGGAGACAGGGATATGAAGGCTGCATTACCTGCAACAGAACGGCCACTTCAAGG 360
DB	702 TGGACACTCTGCTGGGAGACAGGGATATGAAGGCTGCATTACCTGCAACAGAACGGCCACTTCAAGG 761
QY	361 AAGAACAGTCAACATTGCTGCGATGCTGGACTACCTGAGAACCTTGCAAGG 420
DB	762 AAGAACAGTCAACATTGCTGCGATGCTGGACTACCTGAGAACCTTGCAAGG 821
QY	421 AGGGCATCATCACAGGGATATGAAGGCTGCATTACCTGACGAACATGGGCACG 480
DB	822 AGGGCATCATCACAGGGATATGAAGGCTGCATTACCTGACGAACATGGGCACG 881
QY	481 TGCACATCACAGATTCAACATTGCTGCGATGCTGGCACCTGAGATGGGAGACAGATTACACCA 540
DB	882 TGCACATCACAGATTCAACATTGCTGCGATGCTGGCACCTGAGATGGGAGACAGATTACACCA 941
QY	541 TGGCTGGCACCAAGCCATTACATGGCACCTGAGATGGGAGACAGATTACACCA 600

Db 942 TGGCTGGCACCAGCCTTACATGGCACCTGAGATGGTCAGCTCCAGAAAGGAGGGCT 1001
 QY 601 ATTCTTTGCTGTTGACTTGTGGACTTGTGCTGGGATCATGAACTGGCATATGAGGCC 660
 Db 1002 ATTCTTTGCTGTTGACTTGTGGACTTGTGGGATCATGAACTGGCATATGAGGCC 1061
 QY 661 GGAGACCGTATCATATTGGTCCAGTACTTCCAGGAAGGAATTGGTACACAGCTTGAGA 720
 Db 1062 GGAGACCGTATCATATTGGTCCAGTACTTCCAGGAAGGAATTGGTACACAGCTTGAGA 1121
 QY 721 CGACTGTTGTAACCTACCCCTCTGCCTGGTCAACAGGAATGGTCACTTAAAGGC 780
 Db 1122 CGACTGTTGTAACCTACCCCTCTGCCTGGTCAACAGGAATGGTCACTTAAAGGC 1181
 QY 781 TACTGAAACCTAATCCAGACCAACGATTTCTCAAGTTATCTGATGTCAGAACCTCCCGT 840
 Db 1182 TACTGAAACCTAATCCAGACCAACGATTTCTCAAGTTATCTGATGTCAGAACCTCCCGT 1241
 QY 841 ATATGAATGATAATAACTCGGGATGCCAGTTTTCAGAAAGGGCTCATTCCAGGTTTCATTTC 900
 Db 1242 ATATGAATGATAATAACTCGGGATGCCAGTTTTCAGAAAGGGCTCATTCCAGGTTTCATTTC 1301
 QY 901 CTAATAAAAGGCAGGCTGAATTGTGATCCTACCTTGAAACTTGAGGAATGGATTGGAGT 960
 Db 1302 CTAATAAGGCAGGCTGAATTGTGATCCTACCTTGAAACTTGAGGAATGGATTGGAGT 1361
 QY 961 CCAAACCTCTACATAAGAAAAAGCGTCTGGCAAAGGAGGATATGGAAAT 1020
 Db 1362 CCAAACCTCTACATAAGAAAAAAAGGCTCTGGCAAAGGAGGATATGGAAAT 1421
 QY 1021 GCGGATTCTCTCAGACATGCTCTTCAGACATGCTCTTCAGAAAGGAGGTTCA 1080
 Db 1422 GCGGATTCTCTCAGACATGCTCTTCAGACATGCTCTTCAGAAAGGAGGTTCA 1481
 QY 1081 TAATTTCACAGAGAAAAGTAAACAGGACTTTAACAAAGACAACCAAATCTAGCCT 1140
 Db 1482 TAATTTCACAGAGAAAAGTAAACAGGACTTTAACAAAGACAACCAAATCTAGCCT 1541
 QY 1141 TGGAAACAAACCAAGGACCCACAAGGTAGGGATGGTCAGAATAACAACTGTAA 1193
 Db 1542 TGGAAACAAACCAAGGACCCACAAGGTAGGGATGGTCAGAATAACAACTGTAA 1594

RESULT 5
 AAD34317
 ID AAD34317 standard; cDNA; 1594 BP.
 XX AC AAD34317;
 XX DT 16-JUL-2002 (First entry)
 DE Human PKIN-20 cDNA.
 XX KW Human; kinase; enzyme; PKIN-20 protein; immune system disorder; anaemia; acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease; asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease; AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; Down's syndrome; gene therapy; protein therapy; cytostatic; gene; ss.
 XX OS Homo sapiens.
 XX PH Key
 PT CDS Location/Qualifiers
 FT /*tag= a
 FT /product= "Human PKIN-20 protein"
 XX WO200218557-A2.
 XX 07-MAR-2002.
 PD 31-AUG-2001; 2001WO-US027219.
 XX PF 31-AUG-2001; 2001WO-US027219.

PR 31-AUG-2000; 2000US-0229873P.
 PR 08-SEP-2000; 2000US-0231357P.
 PR 14-SEP-2000; 2000US-0232654P.
 PR 22-SEP-2000; 2000US-0234902P.
 PR 29-SEP-2000; 2000US-0236499P.
 PR 06-OCT-2000; 2000US-0238389P.
 PR 13-OCT-2000; 2000US-0240542P.
 XX PA (INCY-) INCYTE GENOMICS INC.
 XX PI Bandman O, Nguyen DB, Walia NK, Hafalia AJA, Yao MG, Gandhi AR;
 PI Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM;
 PI Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT;
 PI Azimzai Y, Burrihill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG;
 PI Ramkumar J, Warren BA, Kearney JL, Thangavelu K;
 PI Burford N;
 XX DR WPI; 2002-329769/36.
 DR P-PSDB; AAE21725.
 XX PT New human kinases, useful for diagnosing, treating or preventing immune system disorders (e.g. Crohn's disease), neurological disorders (e.g. epilepsy), or cell proliferative disorders (e.g. cancers such as leukemia or lymphoma).
 XX PS Claim 99; Page 214; 218pp; English.
 XX CC The present invention relates to human kinases (PKIN) and polynucleotides encoding such proteins. PKIN sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of PKIN, particularly immune system disorders (e.g. acquired immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease, anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-Tooth disease or seizures), cell proliferative disorders (e.g. cancers such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma), and developmental disorders (e.g. Down's syndrome). They are also used in gene therapy and protein therapy. The present sequence is a cDNA encoding human PKIN-20 protein.
 XX SQ Sequence 1594 BP; 441 A; 386 C; 395 G; 372 T; 0 U; 0 Other;
 Query Match Score 1188.2; DB 6; Length 1594;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1190; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CCATGGGAGGCGAACCTTCAGAAAAACCCAGTCTGAAATGGAGATGTCAACT 60
 Db 402 CCATGGGAGGCCAACCTTCAGAAAAACCCAGTCTGAAATGGAGATGTCAACT 461
 QY 61 TTGACCACTTTGAAATTGGGAAAGGAGTTGGGAGGCTCTGCATTTG 120
 Db 462 TTGACCACTTTGAAATTGGGAGGCTCTGCATTTG 521
 QY 121 TACAGAAGAAATGATAACAGAAAGATGTGCAATGAAAGTACATGAAATAACAAAGTGCG 180
 Db 522 TACAGAAGAAATGATAACAGAAAGATGTGCAATGAAAGTACATGAAATAACAAAGTGCG 581
 QY 181 TGGAGGCCAATGAGAAATGCTTCAGAAACTCCAGATCATGGGGCTGGAGC 240
 Db 582 TGGAGGCCAATGAGAAATGCTTCAGAAACTCCAGATCATGGGGCTGGAGC 641
 QY 241 ACCCTTTCCTGGTTAATTGGCTTCTCCAAAGATGAGGAAGATGGTCATGGTGG 300
 Db 642 ACCCTTTCCTGGTTAATTGGCTTCTCCAAAGATGAGGAAGATGGTCATGGTGG 701
 QY 301 TGGACCTCCTGGGGAGACCTGGCTTATCACCTGCAACAGAACGGTCACTTCAGG 360
 Db 702 TGGACCTCCTGGGGAGACCTGGCTTATCACCTGCAACAGAACGGTCACTTCAGG 761
 QY 361 AAGAAACAGTGAAGGTCTTCATCTGTGAGCTGCTGGCTCATGGCTGAGAAC 420
 Db 762 AAGAAACAGTGAAGGTCTTCATCTGTGAGCTGCTGGCTCATGGCTGAGAAC 821

Db	361	GAAACAGTGAAGCTTCATCTGTGAGCTGGCTCAATGGCCATGGACTACCTGGAGAACCCAG	420	PN WO2001B15557-A2.
Qy	423	CGCATCATTCAAGGGATATGAAAGCTGACAATATTTTACTTGACGAACATGGGCACCGTG	482	XX 01-NOV-2001.
Db	421	CGCATCATTCAAGGGATATGAAAGCTGACAATATTTTACTTGACGAACATGGGCACCGTG	480	PD XX
Qy	483	CACATCACAGATTCAACATTGCTGCGATGCTGCCAGGGAGACACAGMATTACCACTG	542	PP 24-APR-2001; 2001WO-US013149.
Db	481	CACATCACAGATTCAACATTGCTGCGATGCTGCCAGGGAGACACAGMATTACCACTG	540	XX
Qy	543	GCTGGCACCAAGCCTTACATGGCACCTGAGATGTCAGCTCAGAAACGGAGGCTAT	602	PR 25-APR-2000; 2000US-019499P.
Db	541	GCTGGCACCAAGCCTTACATGGCACCTGAGATGTCAGCTCAGAAACGGAGGCTAT	600	PR 01-MAY-2000; 2000US-0201227P.
Qy	603	TCCTTGTGTCAGTGGTACTTCAGCAAGGAATATGTACACACGTTGAGACG	722	XX
Db	601	TCCTTGTGTCAGTGGTACTTCAGCAAGGAATATGTACACACGTTGAGACG	720	PA (LEXI-) LEXICON GENETICS INC.
Qy	663	AGACCGTATCATATTGCTCCAGTACTTCAGCAAGGAATATGTACACACGTTGAGACG	722	XX
Db	661	AGACCGTATCATATTGCTCCAGTACTTCAGCAAGGAATATGTACACACGTTGAGACG	720	PS Disclosure; Page 44; 44pp; English.
Qy	723	ACTGTTGTAACCTACCCCTCTGCTGCTGCAAGGAATGGTGTCACTCTAAAGCTA	782	XX
Db	721	ACTGTTGTAACCTACCCCTCTGCTGCTGCAAGGAATGGTGTCACTCTAAAGCTA	780	CC The invention relates to novel human protein (NHP) kinases and their corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as pharmaceutical reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. NHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, the treatment of physiological disorders or diseases, and cosmetic and nutraceutical applications. NHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular chromosome. NHP DNA is further useful as hybridisation probes for screening libraries and assessing gene expression patterns, and also for the detection of mutant NHPs or inappropriately expressed NHPs for disease diagnosis. NHP DNA is also useful in gene therapy. The present sequence is novel human protein (NHP) kinase full-length ORF (open reading frame) and flanking region DNA related to the invention
Qy	783	CTCGAACCTAAATCCAGAACCAACGATTCTCCGTATCTGATGTCCAGAACACTTCGGTAT	842	XX
Db	781	CTCGAACCTAAATCCAGAACCAACGATTCTCCGTATCTGATGTCCAGAACACTTCGGTAT	840	CC
Qy	843	ATGATGATAAACTGGATGGCAGTTTCAGAAAGGGCTCATCCAGGGTTCATTCCT	902	CC
Db	841	ATGATGATAAACTGGATGGCAGTTTCAGAAAGGGCTCATCCAGGGTTCATTCCT	900	CC
Qy	903	AATAAAGGCACGCTGAATTGTCAGTCTACCTTGTGAACTTGGAATTTGGAGTCC	962	CC
Db	901	AATAAAGGCACGCTGAATTGTCAGTCTACCTTGTGAAATGATTGGAGTCC	960	CC
Qy	963	AAACCTCTACATAAGAAAAAGGGCTCTGACTCTGGCAAAAGAAGGGATATGGAAATGC	1022	XX
Db	961	AAACCTCTACATAAGAAAAAGGGCTCTGACTCTGGCAAAAGAAGGGATATGGAAATGC	1020	Query Match 78.3%; Score 1162.6%; DB 6; Length 1675;
Qy	1023	GATTCTCTCAGACATGTCTTCAAGGACCTTGACTCTGTCCAGAAGGGTTCTATA	1082	Best Local Similarity 98.8%; Pred. No. 6.7e-312;
Db	1021	GATTCTCTCAGACATGTCTTCAAGGACCTTGACTCTGTCCAGAAGGGTTCTATA	1080	Mismatches 0; Indels 0; Gaps 0;
Qy	1083	ATTTCAACAGAGAAAAAGTAAACAGGGACTTTAACAAAAGAACCAAAATCTAGCCTTG	1142	Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Db	1081	ATTTCAACAGAGAAAAAGTAAACAGGGACTTTAACAAAAGAACCAAAATCTAGCCTTG	1140	QY 1 CCATGGGAGGCAACACTTCAGAAATGGCAGCTTGGGAGGGCTGGCATCTGCAACT 60
Qy	1143	GAACAAACCAAGAACCCACAAAGGTGAGGAATGGTCAGAATAAACAAACTTGTAA	1193	Db 411 CCATGGGAGGCAACACTTCAGAAATGGCAGCTTGGGAGGGCTGGCATCTGCAACT 470
Db	1141	GAACAAACCAAGAACCCACAAAGGTGAGGAATGGTCAGAATAAACAAACTTGTAA	1191	QY 61 TTGACCACTTGAATTTGGCAGCCATTGGGAAAGGCAGTTGGGAAAGGTCTGCATCTGCAACT 120
Qy	181	TGACAGAATGATAACCAAGAAGATGTGGCAATGTAAGTACATGAATAAACAAAGTGC	180	Db 471 TTGACCACTTGAATTTGGCAGCCATTGGGAAAGGTCTGCATCTGCAACT 530
Db	180	TACAGAAGAATGATAACCAAGAAGATGTGGCAATGTAAGTACATGAATAAACAAAGTGC	180	QY 121 TACAGAAGAATGATAACCAAGAAGATGTGGCAATGTAAGTACATGAATAAACAAAGTGC
Qy	531	TACAGAAGAATGATAACCAAGAAGATGTGGCAATGTAAGTACATGAATAAACAAAGTGC	590	Db 531 TACAGAAGAATGATAACCAAGAAGATGTGGCAATGTAAGTACATGAATAAACAAAGTGC
Qy	181	TGGAGGGCAATGAGTCAGAAATGTCCTCAAGGAACATGAGTCATGGGGCTGGAGC	240	QY 181 TGGAGGGCAATGAGTCAGAAATGTCCTCAAGGAACATGAGTCATGGGGCTGGAGC
Db	591	TGGAGGGCAATGAGTCCTGGTCAATCTGTGAGCTGGAGACCTGGCTGGAGTCATGGGG	300	Db 591 ACCCTTCTGGTCAATCTGTGAGCTGGAGACCTGGCTGGAGTCATGGGGCTGGAGC
Qy	241	ACCCTTCTGGTCAATCTGTGAGCTGGAGACCTGGCTGGAGTCATGGGGCTGGAGC	360	QY 241 ACCCTTCTGGTCAATCTGTGAGCTGGAGACCTGGCTGGAGTCATGGGGCTGGAGC
Db	711	TGGAGGGCAATGAGTCCTGGTCAATCTGTGAGCTGGAGACCTGGCTGGAGTCATGGGG	420	Db 711 ACCCTTCTGGTCAATCTGTGAGCTGGAGACCTGGCTGGAGTCATGGGGCTGGAGC
Qy	361	AAGAAACAGTGAAGCTCTGCTCATCTGTGAGCTGGAGACCTGGCTGGAGTCATGGGG	420	QY 361 AAGAAACAGTGAAGCTCTGCTCATCTGTGAGCTGGAGACCTGGCTGGAGTCATGGGG
Db	771	AAGAAACAGTGAAGCTCTGCTCATCTGTGAGCTGGAGACCTGGCTGGAGTCATGGGG	830	Db 771 AAGAAACAGTGAAGCTCTGCTCATCTGTGAGCTGGAGACCTGGCTGGAGTCATGGGG
Qy	421	AGGGCATCATTCAACAGGGATATGAGGCTGACATTTTACRTGACGAAATGGGGACG	480	QY 421 AGGGCATCATTCAACAGGGATATGAGGCTGACATTTTACRTGACGAAATGGGGACG

Db 831 AGGGCATCATTACAGGGATATGAAGCTGACAATATTACTTGTACCACTGGGCCACG 890 XX WO200181557-A2.
 QY 481 TGCACATCACAGATTCAACATTGCTGGATGTCGCCAGGGAGCACAGATTACCCA 540 XX PD 01-NOV-2001.
 Db 891 TGCACATCACAGATTCAACATTGCTGGATGTCGCCAGGGAGCACAGATTACCCA 950 XX PF 24-APR-2001; 2001WO-US013149.
 QY 541 TGGCTGGACCAAGCCTTACATGGGACTCTGAGATGTTCAAGCTCCAGGAGGAGGCT 600 XX PR 25-APR-2000; 2000US-0199499P.
 Db 951 TGGCTGGACCAAGCCTTACATGGGACTCTGAGATGTTCAAGCTCCAGAAGGAGGCT 1010 XX PR 01-MAY-2000; 2000US-0201227P.
 PA (LEXI-) LEXICON GENETICS INC.
 QY 601 ATTCCTTGTGTTGACTGGTGGTCCCTGGAGTGACGGCATATGAACACTGCTGAGAGGCC 660 XX PI Hu Y, Nepomnych B, Wang X, Donoho G, Scoville J, Walko DW;
 Db 1011 ATTCCATTGTGTTGACTGGTGGTCCCTGGAGTGACGGCATATGAACACTGCTGAGAGGCC 1070 XX DR WPI; 2002-034442/04.
 QY 661 GGAGACCGTATCATATTGGTCCAGTACTTCCAGGAAGAAATTGATGACACAGTTGAGA 720 DR P-PSDB; AAB14260.
 Db 1071 GGAGACCGTATCATATTGGTCCAGTACTTCCAGGAAGAAATTGATGACACAGTTGAGA 1130 XX
 QY 721 CGACTGTTGAACTTACCCCTCTGCCTGGTACAGGAATGCTGGTCACTCTAAAGGC 780 PT New nucleic acid molecules encoding new human proteins, useful in
 Db 1131 CGACTGTTGAACTTACCCCTCTGCCTGGTCACTCTAAAGGC 1190 PT diagnosis, drug screening, clinical trial monitoring, treatment of
 PT physiological disorders, and cosmetic or nutriceutical applications.
 PS Claim 4; Page 41; 44pp; English.
 XX
 CC The invention relates to novel human protein (NHP) kinases and their
 CC corresponding cDNA molecules. NHP kinase and its DNA are useful as
 CC reagents in assays for screening compounds that can be used as
 CC pharmaceutical reagents useful in the therapeutic treatment of mental,
 CC biological and medical disorders, and also as chemotherapeutic agents
 CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is
 CC useful for diagnosis, drug screening, clinical trial monitoring, the
 CC treatment of physiological disorders or diseases, and cosmetic and
 CC nutriceutical applications. NHP DNA is also useful for the identification
 CC of coding sequence and the mapping of a unique gene to a particular
 CC chromosome. NHP DNA is further useful as hybridisation probes for
 CC screening libraries and assessing gene expression patterns, and also for
 CC the detection of mutant NHPs or inappropriately expressed NHPs for
 CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
 CC sequence is novel human protein (NHP) kinase which is similar to
 CC serine/threonine protein kinases, ribosomal protein kinases and cAMP-
 CC dependent kinases cDNA related to the invention.
 SQ Sequence 1224 BP; 381 A; 263 C; 283 G; 297 T; 0 U; 0 Other;
 Query Match 78.2%; Score 1160.6; DB 6; Length 1224;
 Best Local Similarity 98.8%; Pred. No. 2.1e-311;
 Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 QY 3 ATGGGAGCGAACCTTCAGAAAACCACAGTGGCTGAAAGATGTCAACTTT 62
 Db 1191 TACTCGAACCTTAATCCAGAACGATTTCTCAGTTATCTGATGTCCAGAACCTCCCGT 1250
 QY 841 ATATGAATGATAAACTGGATGCAAGGTTTCAGTTCACTGGCTCATTCATTC 900
 Db 1251 ATATGAATGATAAACTGGATGCAAGGTTTCAGAAAGGGCTCATTCATTC 1310
 QY 901 CTAATAAAGGGAGGCTGAAATTGTTGATCTTACCTTGAACTTGGAGT 960
 Db 1311 CTAATAAAGGGAGGCTGAAATTGTTGATCTTACCTTGAACTTGGAGT 1370
 QY 961 CCAAACCTCTACATAAGAAAAAAAGCTCTGGCAAAGGAAGGATATGACCAAT 1020
 Db 1371 CCAAACCTCTACATAAGAAAAAAAGCTCTGGCAAAGGAAGGATATGACCAAT 1430
 QY 1021 GCGATTCCTCTCAAGACATGTCTTCAAGAGGCCCTTGACTCTGTCCAGGAAGGGACTTCA 1080
 Db 1431 GCGATTCCTCTCAAGACATGTCTTCAAGAGGCCCTTGACTCTGTCCAGGAAGGGACTTCA 1490
 QY 1081 TAATTCTAACAGAGAAAAGTAAACAGGGACTTAACAAAGACAACCAAATCTAGCCT 1140
 Db 1491 TAATTCTAACAGAGAAAAGTAAACAGGGACTTAACAAAGACAACCAAATCTAGCCT 1550
 QY 1141 TGGAAACAACCAAGACCCACAAGGTGAGGATGGTCAAGATAACA 1185
 Db 1551 TGGAAACAACCAAGACCCACAAGGTGAGGATGGTCAAGATAACA 1595
 RESULT 8
 ID AAD23678 standard; cDNA; 1224 BP.
 XX DE Novel human protein (NHP) kinase cDNA #3.
 XX KW Novel human protein; NHP; gene therapy; diagnosis; drug screening;
 KW gene expression; breast cancer; prostate cancer; nutriceutical; cosmetic;
 KW medical disorder; mental; biological; physiochemical; chemotheapeutic;
 KW ss.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FT 1. 1224
 FT /* tag= a /product= "Novel human protein (NHP) kinase"
 FT 422
 DB 303 GACCTCCCTGCTGGTGGAGACCTCATGGCTCATGGTGAAGCTTCAAGGAA 362
 DB 301 GACCTCCCTGCTGGTGGAGACCTCATGGCTCATGGTGAAGCTTCAAGGAA 360
 QY 363 GAAACAGTGAAGGCTTCAAGGAACTTCAAGGAACTTCAAGGAA 362

Db 361 GAAACAGTGAAGCTCTTCATCTGTGAGCTGGCTGGACTACCTGGAGAACCCAG 420
 Qy 423 CGCATTCATTCAAGGGATATGAGAAGCTGACAATTTTACTTGACGAAACATGGCCAAGTG 482
 Db 421 CGCATTCATTCAAGGGATATGAGCCTGACAATTTTACTTGACGAAACATGGGCCAGTG 480
 Qy 483 CACATCACAGATTCAACATTGCGATGCTGCCAGGGACACAGATTACCAACATG 542
 Db 481 CACATCACAGATTCAACATTGCGATGCTGCCAGGGACACAGATTACCAACATG 540
 Qy 543 GCTGGCACAGCCTTACATGGCACCTAGCTCAGAAAAGGGAGGAGGCTAT 602
 Db 541 GCTGGCACAGCCTTACATGGCACCTAGCTCAGAAAAGGGAGGAGGCTAT 600
 Qy 603 TCCTTGGTGTGACTGGTGGTCCCTGGACTGACGGCCATATGAACTGGCTGAGGGCCGG 662
 Db 601 TCCTTGGTGTGACTGGTGGTCCCTGGACTGAGATGTTAGCTGAGGGCATATGAGGGCCGG 660
 Qy 663 AGACCGTATCATATTGCTCCAGTACTCCAGGAAGGAATTGTACACACAGTTGAGACG 722
 Db 661 AGACCGTATCATATTGCTCCAGTACTCCAGGAAGGAATTGTACACGTGAGACG 720
 Qy 723 ACTGTTGTAACCTTACCCCTTGCCCTGTCAGGAAATGGTCTCACTTCTAAAGCTA 782
 Db 721 ACTGTTGTAACCTTACCCCTTGCCCTGTCAGGAAATGGTCTCACTTCTAAAGCTA 780
 Qy 783 CTGGRACCTTAATCCAGACCAACGATTTCCTCAGTTATCTGATGTCAGACTTCCCGTAT 842
 Db 781 CTCGAACCTTAATCCAGACCAACGATTTCCTCAGTTATCTGATGTCAGACTTCCCGTAT 840
 Qy 843 ATGAATGATAATAACTGGATGCACTTCAAGAAGGGCTCATTCAGGTTCATTCCT 902
 Db 841 ATGAATGATAATAACTGGATGCACTTCAAGAAGGGCTCATTCAGGTTCATTCCT 900
 Qy 903 AATAAAGGCAGGCTGAATTGTGATCCATCCTTGAACCTTGAACTTGAAGGATGGTCC 962
 Db 901 AATAAAGGCAGGCTGAATTGTGATCCATCCTTGAACCTTGAACTTGAAGGAAATGTC 960
 Qy 963 AAACCTCTACATAAGAAAAAAAGGCTGTCAGGAAAGGAAGGAAAGGAAATGTC 1022
 Db 961 AAACCTCTACATAAGAAAAAAAGGCTGTCAGGAAAGGAAGGAAAGGAAATGTC 1020
 Qy 1023 GATTCTCTCAAGACATGTCTCTCAAGAGGCACCTGACTCTGTCAGAAGGAGTTCTATA 1082
 Db 1021 GATTCTCTCAAGACATGTCTCTCAAGAGGCACCTGACTCTGCAAGAAGGAGTTCTATA 1080
 Qy 1083 ATTTCACAGAGAAAAGTAAACAGGGACTTTAACAAAGGAAACCAAATCTAGCCCTTG 1142
 Db 1081 ATTTCACAGAGAAAAGTAAACAGGGACTTTAACAAAGGAAACCAAATCTAGCCCTTG 1140
 Qy 1143 GAAACAAACCAAGACCCACAAAGGTGAGGATGGTCAGAATAACA 1185
 Db 1141 GAAACAAACCAAGACCCACAAAGTGACAAATGGCAAAATGGCA 1183
 RESULT 9
 AAS06704 ID AAS06704 standard; cDNA; 981 BP.
 XX AC AAS06704;
 XX DT 12-SEP-2001 (first entry)
 DE Polynucleotide sequence encoding human protein kinase #4.
 XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder; gene therapy; ss.
 XX Homo sapiens.
 PN WO200138503-A2.

XX PD 31-MAY-2001.
 XX PR 24-NOV-1999; 99US-0167482P.
 XX PA (SUGB-) SUGEN INC.
 XX PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Blanigan P, Clary D;
 XX DR 2001-343950/36.
 XX PT Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX PS Example 1; Fig 1; 433pp; English.
 XX CC AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate kinase expression. For example, they may be used to treat
 CC cancers (especially cancers of haemopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be used for
 CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
 CC polypeptides may be used as antigens in the production of antibodies
 CC against the protein kinases and in assays to identify modulators of
 CC protein kinase expression and activity.
 XX SQ Sequence 981 BP; 294 A; 207 C; 235 G; 245 T; 0 U; 0 Other;
 Query Match 56.0%; Score 831.2; DB 4;
 Best Local Similarity 90.7%; Pred. No. 5.2e-220;
 Matches 903; Conservative 0; Mismatches 78; Indels 15; Gaps 1;
 Db QY 3 ATGGGAGGCGAACACTTCAGAAAAACCAACAGTTGTTGATGAAAGATGTCAACTT 62
 Db QY 1 ATGGGAGGCGAACACTTCAGAAAAACCAACAGTTGTTGATGAAAGATGTCAACTT 60
 Db QY 63 GACCACTTTGAAATTGGCGAGCCATTGGGAAAGGCAATTGGGAGGTTCTGCATTGTA 122
 Db QY 61 GACCACTTTGAAATTGGCGAGCCATTGGGAAAGGCAATTGGGAGGTTCTGCATTGTA 120
 Db QY 123 CAGAAGGAATGATAACCAAGAAGATGTGCGCAATGAAGGATCATGATAAAAGTGCCTG 182
 Db QY 121 CAGAAGGAATGATAACCAAGAAGATGTGCGCAATGAAGGATCATGATAAAAGTGCCTG 180
 Qy 183 GAGCGCAATGAAACTGAGAAATGTCCTTCAAGGAAAGACATGGCTGGAGGAC 242
 Db 181 GAGCGCAATGAAAGTGGAAATGTCCTTCAAGGAAAGACATGGCTGGAGGAC 240
 Qy 243 CCTTTCTGGTTAATTGGTTATTCCCTTCAGGAAATGAGGAAAGACATGGCTGG 302
 Db 241 CCTTTCTGGTTAATTGGTTATTCCCTTCAGGAAATGAGGAAAGACATGGCTGG 300
 Qy 303 GACCTCTGCTGGTGGAGACCTGGTTATCACCTGCAACAGAACGTCCACTTCAGGAA 362
 Db 301 GACCTCTGCTGGTGGAGACCTGGTTATCACCTGCAACAGAACGTCCACTTCAGGAA 360
 Qy 363 GAAACAGTGAAGCTCTTCATCTGTGAGGTGGCTCATGGCCCTGGACTACCTGGAGAAC 422
 Db 361 GAAACAGTGAAGCTCTTCATCTGTGAGGTGGCTCATGGCCCTGGAGAAC 420

QY	423 CGCATCATTCAAGGGATATGAAAGCTGACAATTTTACTTGACRAACATGGCACAGTG 482	PR 03-FEB-2000; 2000US-00496914.
Db	421 CGCATCATTCAAGGGATATGAAAGCTGACAATTTTACTTGACRAACATGGCACAGTG 480	PR 27-APR-2000; 2000US-00560875.
QY	483 CACATCACAGATTCAACATTCGCTGCATGGCCAGGGAGACACAGATTACCCATG 542	XX PA (HYSEQ INC.
Db	481 CACATCACAGATTCAACATTCGCTGCATGGCCAGGGAGACACAGATTACCCATG 540	XX PI Tang YT, Liu C, Drmanac RT;
QY	543 GCTGGCACCAAGCCTTACATGGCACCTGACTGGTGTGAGATGTTCAAGCTCOAGAAAAGGAGCAGGCTAT 602	XX WPI; 2001-457740/49.
Db	541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAAGCTCOAGAAAAGGAGCAGGCTAT 600	DR P-PSDB; ABB11219.
QY	603 TCCTTGTGTTGACTGGTGTGAGATGTTCAAGCTCOAGAAAAGGAGCAGGCTAT 662	XX Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer.
Db	601 TCCTTGTGTTGACTGGTGTGAGATGTTCAAGCTCOAGAAAAGGAGCAGGCTAT 660	XX PS Claim 1; Page 422; 1963pp; English.
QY	663 AGACCGTATCATATTGCTCCAGTACTTCCAGGAATTGTCACACGTTTGAGACG 722	XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
Db	661 AGACCGTATCATATTGCTCCAGTACTTCCAGGAATTGTCACACGTTTGAGACG 720	XX haematopoiesis regulatory activity; tissue growth activity;
QY	723 ACTGTGTAACTTACCCCTCTGGTCACAGGAATGGTCACTTCTTAAGGCTA 782	XX immunomodulatory activity; activin- or inhibin-related activities;
Db	721 ACTGTGTAACTTACCCCTCTGGTCACAGGAATGGTCACTTCTTAAGGCTA 780	XX chemotactic or chemoattract activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.
QY	783 CTCGAACCTAACCCAGACCACGATTCTCAGTTATCTGATGTCAGACTTCCCCTAT 842	XX Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders.
Db	781 AGAAGGAAGACTGCATGTG-.....CAAACGAAGTAACAAAGGAAGCAGG 825	XX Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
QY	843 ATGAATGATAAAACTGGATGCGAGTTTCAGAAGAGGCTCATTCCAGGTTTCATTCTC 902	XX SQ Sequence 678 BP; 203 A; 148 C; 175 T; 0 U; 0 Other;
Db	826 CTCTCTGGCTTAAGTTAGAAGTTAGTATAATTTGGGACACCAACTGTCTTCCTTG 885	XX Query Match 45.3%; Score 672.8; DB 4; Length 678;
QY	903 AATAAAGGCCAGGTGAATTCTGATCCTACCTTGAACCTGAGGAATATGATTGGAGTCC 962	XX Best Local Similarity 99.7%; Pred. No. 4.1e-176;
Db	886 CAGAAAGCCAGGTGAATTGTGATCCTACCTTGAACCTGAGGAATATGGAGTCC 945	XX Matches 674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	963 AAACCTCTACATAGAAAAAGGCTCTGGCAAAG 998	QY 441 ATGAAAGCTGTGACATATTTCATTGACCGAACATCACAGATTTCAC 500
Db	946 AAACCTCTACATAGAAAAAGGCTCTGGCAAAG 981	Db 1 ATGAAAGCTGTGACATATTTCATTGACCGAACATCACAGATTTCAC 60
RESULT 10		QY 501 ATGGCACCTGAGATGTTCAAGCTCCAGAAAAGGAGACACAGATTACCCATGGCTGGCACCAAGCCTTAC 560
ID ABA08463 standard; cDNA; 678 BP.		Db 61 ATGCTGGATGCTGCCAGGGAGACAGATTACCCATGGCTGGCACCAAGCCTTAC 120
XX ABA08463		QY 561 ATGGCACCTGAGATGTTCAAGCTCCAGAAAAGGAGACACAGATTACCCATGGCTGGCACCAAGCCTTAC 620
DT 11-JAN-2002 (first entry)		Db 121 ATGGCACCTGAGATGTTCAAGCTCCAGAAAAGGAGACAGATTACCCATGGCTGGCACCAAGCCTTAC 180
XX Human Ser/Thr kinase homologue-encoding cDNA, SEQ ID NO: 239.		QY 621 TGGTCCCTGGGAGTGAAGGCATATGAACCTGAGGGGGAGACCGTATATTCCGC 680
KW Human; cytokine; cell proliferation; cell differentiation; growth factor; haemopoiesis regulation; tissue growth; immunomodulator; activin; inhibitor; chemotaxis; chemokinesis; thrombolytic condition; proliferative retinopathy; arterial ischaemia; oncogenesis; myeloid cell disorder; lymphoid cell disorder; tumour; haematopoietic disorder; atherosclerosis; coronary heart disease; bone disorder; osteoporosis; vascular growth disorder; infection; immune disorder; tissue regeneration; wound healing; antiinflammatory; cell culture; drug screening; gene therapy; antiarthritic; antiasthmatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; viricide; antibacterial; antifungal; pulmonary; antiulcer; ss.		
DE Homo sapiens.		
XX WO200157188-A2.		
XX 09-AUG-2001.		
XX 05-FEB-2001; 2001WO-US003800.		
XX OS		
XX		
PN		

Qy	181	TGGTCCCTGGGAGGTGACGGCATATGAACACTGCTGAGAGGCCGGAGACCGT 240
Qy	681	TCCAGTACTTCCAGCAAGGAAATTGTACACACCGTTGAGGACTGTTGAACTAACCT 740
Db	241	TCCAGTACTTCCAGCAAGGAAATTGTACACACCGTTGAGGACTGTTGAACTAACCT 300
Qy	741	TCTGCCTGGTCACAGGAATGGTGTCACTTCAAGGCTTAATCAGAC 800
Db	301	TCTGCCTGGTCACAGGAATGGGAACTTCAAGGCTTAATCAGAC 360
Qy	801	CAACGATTTCAGTTCTCAGTTATCTGATGTCCAGAACCTTCCCCTATAGATAACTGG 860
Db	361	CAACGATTTCAGTTCTCAGTTATCTGATGTCCAGAACCTTCCCCTATAGATAACTGG 420
Qy	861	GATGCAGGTTTCAGAACAGGGCTCATTCAGGTTTCATTCCCTAATAAAGGCAGGGCTGAAT 920
Db	421	GATGCAGGTTTCAGAACAGGGCTCATTCAGGTTTCATTCCCTAATAAAGGCAGGGCTGAAT 480
Qy	921	TGTGATCCTACCTTGAACTTGAGGAATTGATTGGAGTCCAAACCTCTACATAAGAA 980
Db	481	TGTGATCCTACCTTGAACTTGAGGAATTGATTGGAGTCCAAACCTCTACATAAGAA 540
Qy	981	AAAAAGCGTCTGGCAAAGGAAGGGATATGAGGAATTGGGAAATGGGATTCTTCTCAGACATGT 1040
Db	541	AAAAAGCGTCTGGCAAAGGAAGGGATATGAGGAATTGGGAAATGGGATTCTTCTCAGACATGT 600
Qy	1041	CttCTTCAAGAGCACCCTGACTCTGTCGCCAGAAGGAGTTCTACAATTTCAACAGAGAAAAA 1100
Db	601	CTTCTTCAAGAGCACCCTGACTCTGTCGCCAGAAGGAGTTCTACAATTTCAACAGAGAAAAA 660
Qy	1101	GTAAAACAGGGACTTTA 1116
Db	661	GTAAAACAGGGACTGTAA 676

RESULT 11
ID AAD23677 standard; cDNA; 711 BP.
XX AAD23677;
AC XX
DT 07-MAR-2002 (first entry)
XX Novel human protein (NHP) kinase cDNA #2.
XX Novel human protein; NHP; gene therapy; diagnosis; drug screening;
KW gene expression; breast cancer; prostate cancer; nutriceutical; cosmetic;
KW medical disorder; mental; biological; physiological; chemotherapeutic;
KW SS.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 1. . 711
FT /*tag= a
FT /product= "Novel human protein (NHP) kinase"
XX PN WO200181557-A2.
XX PD 01-NOV-2001.
XX PP 24-APR-2001; 2001WO-US013149.
XX PR 25-APR-2000; 2000US-0199499P.
PR 01-MAY-2000; 2000US-0201227P.
XX PA (LEXI-) LEXICON GENETICS INC.
XX PI Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walko DW,
XX DR WPI; 2002-034442/04.
DR P-PSDB: AAB14259.

PT New nucleic acid molecules encoding new human proteins, useful in
 PT diagnosis, drug screening, clinical trial monitoring, treatment of
 PT physiological disorders, and cosmetic or nutriceutical applications.
 XX Disclosure; Page 40; 44pp; English.

XX The invention relates to novel human protein (NHP) kinases and their
 CC corresponding cDNA molecules. NHP kinase and its DNA are useful as
 CC reagents in assays for screening compounds that can be used as
 CC pharmaceutical reagents useful in the therapeutic treatment of mental,
 CC biological and medical disorders, and also as chemotherapeutic agents
 CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is
 CC useful for diagnosis, drug screening, clinical trial monitoring, the
 CC treatment of physiological disorders or diseases, and cosmetic and
 CC nutriceutical applications. NHP DNA is also useful for the identification
 CC of coding sequence and the mapping of a unique gene to a particular
 CC chromosome. NHP DNA is further useful as hybridisation probes for
 CC screening libraries and assessing gene expression patterns, and also for
 CC the detection of mutant NHPs or inappropriately expressed NHPs for
 CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
 CC sequence is novel human protein (NHP) kinase cDNA which is similar to
 CC serine/threonine protein kinases, ribosomal protein kinases and cAMP-
 CC dependent kinases cDNA related to the invention

XX Sequence 711 BP; 199 A; 153 C; 181 G; 178 T; 0 U; 0 Other;

Query	Match	Score	DB	Length
	Best Local Similarity	99.5%	No.	1-7e-171;
	Matches	658;	Mismatches	0;
	Conservative	0;	Indels	0;
			Gaps	0
Qy	3	ATGGGAGCGAACACTCAAGAAAACCACAGTTTGATGAAATGAAAGATGTCAACTT	62	
db	1	ATGGGAGGCCAACACTCAAGAAAACCACAGTTTGATGAAATGAAAGATGTCAACTT	60	
Qy	63	GACCACTTTGAAATTGGGCAATTGGGAAAGGCAGTTGGGAGGGTCTGCATTGTA	122	
db	61	GACCACTTTGAAATTGGGCAATTGGGAAAGGCAGTTGGGAAGGGTCTGCATTGTA	120	
Qy	123	CAGAAGAATGATAACAGAAGATGTGCCAATGAAAGTACATGAAATAAAACAAAGT	182	
db	121	CAGAAGAATGATAACAGAAGATGTACGGCAATGAAAGTACATGAAATAAAACAAAGT	180	
Qy	183	GAGGCCAATGAAAGTGAAGATGTCTCAAGGAATGTCTCAAGGAACTCCAGATG	242	
db	181	GAGGCCAATGAAAGTGAAGATGTCTCAAGGAACTCCAGATCATGGGAGGCAAC	240	
Qy	243	CCTTTCTGGTTAATTGGGTATTCTTCCAAAGATGAGGAAGACATGGTTCATGGT	302	
db	241	CCTTTCTGGTTAATTGGGTATTCTTCCAAAGATGAGGAAGACATGGTTCATGGT	300	
Qy	303	GACCTCCTGGGGAGACCTGGGTATCACCTGCAACAGAACGTCCACTTCAGGAA	362	
db	301	GACCTCCTGGGGAGACCTGGGTATCACCTGCAACAGAACGTCCACTTCAGGAA	360	
Qy	363	GAAAACAGTGAAGGCTCTTCATCTGTGAGGCTGACTACCTGGCAGAACCCAG	422	
db	361	GAAAACAGTGAAGGCTCTTCATCTGTGAGGCTGACATTTTACTTGACGAAAC	420	
Qy	423	CGGCATCATTACAGGGATAATGAAAGCCGTGACAATATTTTACTTGACGAAAC	482	
db	421	CGGCATCATTACAGGGATAATGAAAGCCGTGACATTTTACTTGACGAAAC	480	
Qy	483	CACATCACAGATTCAACATGGCTGCGATGGCCAGGGAGACACAGATTACACC	542	
db	481	CACATCACAGATTCAACATGGCTGCGATGGCCAGGGAGACACAGATTACACC	540	
Qy	543	GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAAGCTCCAGAAAGG	602	
db	541	GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTCAAGCTCCAGAAAGG	600	
Qy	603	TCCTTGCTGTTGACTGGCTGCCCTGGGAGGTGACGGCATATGAAACTGCTG	662	

Db	601	TCCTTGCTGTTGACTGGTGTCCCCTGGAGTGACGGCATATGAACTGTCAGAGGCCCGG	660		Matches	657;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
QY	663 A	663			QY	3	ATGGGAGGAAACATTCAAGAAAACCACCACTTCAAGAAAATGAAAGATGTCAACTT	62						
DB	661 A	661			DB	1	ATGGGAGCCTAACATTCAAGAAAACCACCACTTCAAGAAAATGAAAGATGTCAACTT	60						
RESULT 12					QY	63	GACCACTTGAATTTCGAGGCCATTGGAAAGGCCATTGGGAGGTCTGCATTGTA	122						
ID AAD23676	AAD23676 standard; cDNA;	678 BP.			DB	61	GACCACTTGAATTTCGAGGCCATTGGAAAGGCCATTGGGAGGTCTGCATTGTA	120						
XX	AAD23676;				QY	123	CAGAAGAATGATAACCAAGAAGATGTGCGAATGAAGTACATGAATAACAAAGTGCCTG	182						
AC					DB	121	CAGAAGAATGATAACCAAGAAGATGTACGCAATGAATAACAAAGTGCCTG	180						
DT 07-MAR-2002	(first entry)				QY	183	GAGGGCAATGAAAGTGAGAAATGCTTCAGGAACACTCCAGATCATGAGGGTCTGGAGCAC	242						
XX	Novel human protein (NHP) kinase cDNA #1.				DB	181	GAGGGCAATGAAAGTGAGAAATGCTTCAGGAACACTCCAGATCATGAGGGTCTGGAGCAC	240						
KW	Novel human protein; NHP; gene therapy; diagnosis; drug screening;				QY	243	CCFTTCCTGGTAAATTGGTGTATCCTTCAAGATGAGGAACATGTTCATGGTGTG	302						
KW	Gene expression; breast cancer; prostate cancer; nutriceutical; cosmetic;				DB	241	CCFTTCCTGGTAAATTGGTGTATCCTTCAAGATGAGGAAGACATGTTCATGGTGTG	300						
KW	medical disorder; mental; biological; physiological; chemotherapeutic;				QY	303	GACCTCCCTGCTGGGGAGACCTGGGAGACCTGGGATACCTGCAACAGTCCACCTCAAGGAA	362						
KW	ss.				DB	301	GACCTCCCTGCTGGGGAGACCTGGGATACCTGCAACAGTCCACCTCAAGGAA	360						
OS Homo sapiens.					QY	363	GAAACAGTGAAGCTCTTCATCTGTGAGGTGTCAATGGCCCTGGACTACCTGCAAAACCAAG	422						
XX	Key CDS	Location/Qualifiers			DB	361	GAAACAGTGAAGCTCTTCATCTGTGAGGTGTCAATGGCCCTGGACTACCTGCAAAACCAAG	420						
FH		1: .678			QY	423	CGCATCATTCAACAGGGATATGAAAGCTGACAATATTACTTACTTGACGAAACATGGCACGTG	482						
FT		/*tag= a			DB	421	CGCATCATTCAACAGGGATATGAAAGCTGACAATATTACTTACTTGACGAAACATGGCACGTG	480						
FT		/product= "Novel human protein (NHP) kinase"			QY	483	CACATCACAGATTCAACATTGCTGGATGCTGCCCAGGGAGAACAGATTACCCATG	542						
FT					DB	481	CACATCACAGATTCAACATTGCTGGATGCTGCCCAGGGAGAACAGATTACCCATG	540						
XX	WO2001181557-A2.				QY	543	GCTGGCCAAGCCATTACATGGCACCTGAGATGTTCAAGTCCAGAAAGGGAGCAGGCTAT	602						
PN					DB	541	GCTGGCCAAGCCATTACATGGCACCTGAGATGTTCAAGTCCAGAAAGGGAGCAGGCTAT	600						
XX	PD 01-NOV-2001.				QY	603	TCCTTTGCTGTTGACTGGTGTCCCTGGGAGTGACGGCATATGAAACTGCTGAGGCCGG	662						
XX	24-APR-2001; 2001WO-US013149.				DB	601	TCCTTTGCTGTTGACTGGTGTCCCTGGGAGTGACGGCATATGAAACTGCTGAGGCCGG	660						
PP														
XX	25-APR-2000; 20000US-0199499P.													
PR														
PR	01-MAY-2000; 20000US-0201227P.													
XX	PA (LEXI-) LEXICON GENETICS INC.													
PI	Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walko DW,													
XX	WPI; 2002-034442/04.													
DR	P-PSDB; AAE14258.													
XX	New nucleic acid molecules encoding new human proteins, useful in													
PT	diagnosis, drug screening, clinical trial monitoring, treatment of													
PT	physiological disorders, and cosmetic or nutriceutical applications.													
XX	PS Disclosure; Page 39; 44pp; English.													
XX	CC The invention relates to novel human protein (NHP) kinases and their													
CC	corresponding cDNA molecules. NHP kinase and its DNA are useful as													
CC	reagents in assays for screening compounds that can be used as													
CC	pharmaceutical reagents useful in the therapeutic treatment of mental,													
CC	biological and medical disorders, and also as chemotherapeutic agents													
CC	useful in the treatment of breast cancer and prostate cancer. NHP DNA is													
CC	useful for diagnosis, drug screening, clinical trial monitoring, the													
CC	treatment of physiological disorders or diseases, and cosmetic and													
CC	nutriceutical applications. NHP DNA is also useful for the identification													
CC	of coding sequence and the mapping of a unique gene to a particular													
CC	chromosome. NHP DNA is further useful as hybridisation probes for													
CC	screening libraries and assessing gene expression patterns, and also for													
CC	the detection of mutant NHPs or inappropriate expressed NHPs for													
CC	disease diagnosis. NHP DNA is also useful in gene therapy. The present													
CC	sequence is novel human protein (NHP) kinase cDNA which is similar to													
CC	serine/threonine protein kinases, ribosomal protein kinases and cAMP-													
CC	dependent kinases cDNA related to the invention													
XX	PS Sequence 678 BP; 195 A; 148 C; 179 G; 156 T; 0 U; 0 Other;													
SQ	Query Match 44.1%; Best Local Similarity 99.5%; Pred. No. 3.2e-171;													

RESULT 13
ABQ61051
ID ABQ61051 standard; CDNA; 1587 BP.
XX ABQ61051;
XX AC
XX DT 26-FEB-2003 (First entry)
XX Serine/threonine kinase encoding sequence.
KW Neuroprotective; immunomodulator; cancer; chromosome 4p16.1-p14;
KW cytostatic; anti-inflammatory; gene therapy; nutritional supplement;
KW wound; burn; ulcer; Alzheimer's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
KW vulnerability; gene; ss.
OS Homo sapiens.
XX PN WO200231111-A2.
XX PD 18-APR-2002.
XX PP 11-OCT-2001; 2001WO-US027760.
XX PR 12-OCT-2000; 2000US-00687527.

PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XXX
DR WPI; 2002-426278/45.
DR N-PSDB; ABP43807.
XXX
PT New polypeptides and their encoded proteins, useful as nutritional
PT sources or supplements, or in gene therapy, particularly for treating
PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
PT inflammation.
XXX
PT Claim 1; SEQ ID # 264; 357pp + Sequence Listing; English.
PT PS

The invention relates to 446 newly isolated polynucleotide sequences. The activity of polynucleotides of the invention may be described as, pulmonary, neuroprotective, immunoprotective, cytostatic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating wounds, burns or ulcers, Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABQ60788-ABQ61233 represent polynucleotides of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

Qy	63	GACCACTTTGAAATTGGCAGGCCATTGGAAAGGGAGGTTCGGGAGGGTCTGCATTTGTA	122
Db	61	GACCATTTCAGATTCTGGCCATTGGTAAAGGGAGTTGGAAAGGTATGCATCGTG	120
Qy	123	CAGAAGATAACCAAGAAGATGTCGCCAATGAAAGTACATGAAATAACAAAAGTGGCTG	182
Db	121	CAGAAGGGAGACACTAAGMAAATGTAATGCAATGAAAGTACATGAACTGGAGCATC	180
Qy	183	GAGGCCAATGAAAGTGAGCAAATGTCCTCAAGGAACACTCCAGATCATGCCAGGTCTGGAGCAC	242
Db	181	GAGAGGGATGAGGGTTCGGAATGTTTCCGGAAATGTCAGATCATGCCAAGGGCTGGAGCAC	240
Qy	243	CCTTCCTGGTTAATTGTTGGTATTCTTCCAAGATGAGGAAGACATGTTCATGGTGGTG	302
Db	241	CCCTTCCTGGTCAATCTGTGGTACTCCTGGTACTCTGGTCAATCTGTGGTCAATCTGTGGT	300
Qy	303	GACCTCCTGGGGAGACCTGGGTTATCACCTGCCAACAGAACGTCACCTCAAGGAA	362
Db	301	GACCTGTCCTGGAGGGGACCTGGGAGGGTACCATCTGCAAGGAAATGTCATGGTCAAGAG	360
Qy	363	GAAACAGTGAAGCTCTTCATCTGTGAGGCTGGTCACTGGCCCTGAGACTACCTGCAAGAACGAG	422
Db	361	GGGACTCTGTGAAACTTCAATCTGTGAGCTGGCACTGGCCCTGAGGTATCTTCAGGGTAC	420
Qy	423	CGCATCATTCAACAGGGATATGAAGGCCGTGACAATATTTCAGGAAACATGGGCACCGTG	482
Db	421	CACATCATTCAACAGGACATCAAGCCAGACAATATCCTGGTGGATGAAACCGGACATGTT	480
Qy	483	CACATCACAGATTCAACATTGCTGCCGATGCTGCCAGGGAGACACAGATTACCACTG	542
Db	481	CACATTACAGACTCAAACATAGCGACGGTAGGTGAAGGGCAGAAAGGGCTTCCTCCATG	540
Qy	543	GCTGGCACCAGGCCATTACATGGCACCTGAGATGTTCAAGGAGGAGGCA-----AGCTCCAGA	596

Db	541	GCTGGCACCAAGCCCTACATGGCTCCAGAACGTTATTCCAGGTCTACATGGACAGGCCCG	600
Qy	597	GGCTTATTCCTTGTGACTGGTCCAGTACTTCCAGGAAATTGGTACACACCGTT	716
Db	601	GGATACTCGTACCCCTGTGACTGGTCCCTGGCATACAGCCTATGAGCTGCGG	660
Qy	657	GGCGGAGACCGTATCATATTGGCTCCAGTACTTCCAGGAAATTGGTACACACCGTT	716
Db	661	GGCTGGGGCTACGGAAATCCACTGGTCAAGGCCATGGTCAAACATGGTTC	720
Qy	717	GAGACGAAGTGTAACTTACCCCTCTGGTCACAGGAATGGTCACTTCTTAAA	776
Db	721	AAGGTGGAGGGTGTCCACTACTCCTCACGGTGCAGGGATGGTGAGGG	780
Qy	777	AAGCTACTCGAACCTAATCCAGAACGATTTCAGTTATCTGATGGTCCAGAACTTC	836
Db	781	AAGCTCCTGACCAAGGATCCTGAGAGCCGGTGTCCAGGCCTCATGACATAAGAGCGTG	840
Qy	837	CCGTATATGAATGATATAACTGGATGGCTCAATTCCAGGCTCAATTCCAGGTTTC	896
Db	841	CCCTACTTGGCGACATGAACTGGGACGGGGTGTCAAGGAAGGCACGTGATGCCCGGCTT	900
Qy	897	ATTCCCTAATAAGGCAGGCTGAAATTGGTACCTTGAACCTTGAGGAATGATTTC	956
Db	901	GTGCCCCAATAAGGGAGGTGAACTGGCATCCACATTGAGCTGATGTTGAAGAGATGTTCA	960
Qy	957	GAGTCCAAACCTCTACATAAGAAAAAAAGCGTCTGGAAAGAA---GGAGAACGGATATG	1013
Db	961	GAATCCAAAGCCACTTCACAAAGAACAGATGGGAAAGAACAGATCCAGGGATGGC	1020
Qy	1014	AGGAATAATGGGATTCTTCAGACATGGTCTTCAAGAGGCACCTTGACTCTGTCCAGAAG	1073
Db	1021	ACAAAGGACAGGCTGCCCGCTGAATGGACACACTGTCAGGCACCTGGAGACTGTTGGAGACTGTCGGGAG	1080
Qy	1074	GAGTTCATATAATTCAACAGAGAAAAAGTAAACAGGAA	1111
Db	1081	GAATTCTCATATTCAACAGAGAACGCTCAGGGCA	1118
RESULT 14			
	AAF44625		
	ID	AAF44625 standard; cDNA; 3224 BP.	
	XX		
	AC	AAF44625;	
	XX	27-MAR-2001 (first entry)	
	DT		
	DB	Novel protein kinase cDNA, SEQ ID NO: 4.	
	XX		
	KW	Human; mouse; protein kinase; antiarthritic; antiesclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.	
	XX	Homo sapiens.	
	OS	WO2000073469-A2.	
	XX	07-DEC-2000.	
	PD		
	PP	26-MAY-2000; 2000WO-US014842.	
	XX	28-MAY-1999; 99US-0136503P.	
	PA	(SUGB-) SUGEN INC.	
	XX	Plowman GD, Martinez R, Whyte D, Sudersanam S;	
	PI		
	XX		
	DR	WPI; 2001-032161/04.	
	DR	P-PSDB; AAB65600.	

Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers.

Example 1: Pig 2; 310pp; English.

The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive diseases.

Sequence 3221: C2U A, 012 C, 183 G, 023 1, 0 U, 0 Other;	Query Match	36.4%	Score 540.8;	DB 4;	Length 3224;
Best Local Similarity		69.1%	Pred. No.	4e-139;	
Matches 772: Congeneriva		0	No. of matches	337;	Indels 0;

3 ATGGGAGCGAACACTTCAGAAAACCACCACTGTTGATGAAATGAAGATGTCAAACCTT 62

125 GACCATTTCAGATTCTGGGCCATTGGTAAAGGGAGTTTGAAAGGTATGCAATCGTG 184

123 CAGAAGGATACCAAGAAGATGTGCCAATGAACTAACAAAAGTGGTG 182

183 CAGAAGCCAGACACTAAGAAAAGTCAAGGATCATGACAAGCAGAAGTCGCAAC 244
183 GAGCCCCAATGAACTGAGAAATTGTCTTCAAGGA&CTCTCCAGATCATTCAGCCCTCTGCACCC 242

245 GAGAGGGATGAGGTTCGGAATGTTTCCGGAGCTGCAGATCATGCCAAGGGCTGGAGCAC 304

243 CCTTCTGGTAATTGTGGTATCCAAAGATGAGGAAGACATGGTGTG 302

303 GACCTCCCTCCACGCCCTTATCACACACCTCCACTTCAACCA 362
305 CCTTTGGTCAATCTGGTACTCTTCAGGATGAGTCACTGGTG 364

365 GACCTGCTCCTGGAGGGACCTGGCTTACCATCTGCAGCAGATGTGCATTTCACAGAG 424

363 GAAACAGTGAAGCTCTCATCTGTGAGCTGGACTACCTGCAGAACCGAG 422

485 CACATCATCCACAGAGACATCAAGGCAAAATCCTGGATGAAACACGGACATGTT 544

483 CACATCACAGATTCAACATTGCCATGCTGCCAGGGAGAACACAGATTACCACTG 542

545 CACATTACAGACTTCAACATAGCGACCGGTAGTGAAAGGAGCAGAAAGGGCTTCCTCCATG 604

605 CCTGGCACCAAGCCCTACATGGCTTACATGGACAGGGCCCC 664

597 GGCTATTCCCTTGCTGTTGACTGGTCCCTGGAGTGACCGCATATGAACCTGCTGAGA 656

Db	665	GGATACTCGTACCCCTGTCGACTGGTGGCTGGCATCACGCCATCACGCCCTGGCTGGC 724
Qy	657	GGCGGAGACCGTATCATATTGCTCCAGTACTTCCAGCTGGTCAAGGAATTGTACACCGTT 716
Db	725	GGCTGGAGGCCGTACGAAATCCCACTCGGTCAACGCCATCGATGAAATCCTCAACATGTT 784
Qy	717	GAGACGACTGTTGTAACCTAACCTTCTGGCTGGTCAAGGAATTGGTGTCACTCTTAAA 776
Db	785	AAGGGAGGGCCGTACGAAATCCCACTCGGTCAACGCCATCGATGAAATCCTCAACATGTT 844
Qy	777	AAGCTACTCGAACCTAATCCAGAACGATTCTCAGTTATCTGATGTCAGAACTTC 836
Db	845	AAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCFTCATGACATAAGGGATG 904
Qy	837	CCGTATATGAATGATATAAACTGGGATGGCAGTTTCAAGAAGGGCTCATTCAGGTTTC 896
Db	905	CCCTACTTGGCGACATGAACACTGGGACGGTGTCAAGAAGGCACTGATGCCGGCTT 964
Qy	897	ATTCCCTAATAAGGCGCTGAAATTGTGATCCTACCTTGAAACTTGAGGAAATGATTTC 956
Db	965	GTGCCAATAAGGGAGGTGAACTGGCATTGGCAACATTGAGATGATTCTA 1024
Qy	957	GAGTCCAAACCTCTACATAAGAAAAAAAGCGTCTGGCAAGA---GGAGAACGATATG 1013
Db	1025	GAATCCAAGGCCACTTCACAAAGAAAGGAGGATTGGCAAAAGAACAGATCCAGGGATGGC 1084
Qy	1014	AGGAATAATGGGATTCTCAGACATGTTCTCAAGAGGCCACCTTGACTCTGTCAGAAG 1073
Db	1085	ACAAGGGACAGCTGCCGGCTGAATGGACACCTGGCAGGACTGTTGGAGACTGTCGGGAG 1144
Qy	1074	GAGTTCATATAAAACAGACAAAAAGTAAACAGGAA 1111
Db	1145	GAATTCATATTCAACAGAGAAAGGCTCAGGAGCA 1182
RESULT 15		
ADA19317	ID	ADA19317 standard; cDNA; 3224 BP.
XX	AC	ADA19317;
XX	DT	20-NOV-2003 (first entry)
XX	DE	Human insulin resistance marker IRM210 (Ser/Thr protein kinase) cDNA #2.
XX	KW	Insulin resistance; IR; susceptibility; diagnosis;
XX	KW	insulin resistance marker; IRM; polymorphism; genotype; hypertension;
XX	KW	dyslipidaemia; type 2 diabetes; obesity; coronary artery disease;
XX	KW	drug screening; antidiabetic; cardiant; antilipaemic; hypotensive; human; gene; ss.
XX	OS	Homo sapiens.
XX	PN	WO20029355-A2.
XX	PD	12-DEC-2002.
XX	PP	03-JUN-2002; 2002WO-US017227.
XX	PR	01-JUN-2001; 2001US-0295264P.
XX	PA	(CLIN-) CLINGENIX INC.
XX	PI	Ma Y, Lih C, Chen F, Fairman J, Chen YI;
XX	DR	WPI; 2003-148601/14.
XX	PT	Diagnosing for insulin resistance (IR) an IR-related condition, e.g.
PT	PT	hypertension, diabetes or obesity, comprises detecting an altered or a
PT	PT	difference in expression of insulin resistance marker (IRM) genes in a
PT	PT	sample from the subject.
PS	Claim 1; Page; 125pp; English.	

The invention relates to a method for diagnosing insulin resistance (IR), an IR-related condition, or susceptibility to IR or an IR-related condition in a patient. The method comprises detecting a difference in expression of at least one insulin resistance marker (IRM) in a biological sample from the patient, compared to the level of expression of the IRM in reference individuals who are not insulin resistant. The invention also encompasses screening for an agent to determine its usefulness in treating IR; the identification of a polymorphism associated with an IR phenotype or risk of developing IR; estimating the frequency of a haplotype for a set of nucleotide polymorphism markers in a population; detecting an association between a haplotype and a phenotype; and identifying genes associated with a disease state. The methods of the invention are useful for diagnosing insulin resistance (IR), an IR-related condition, or susceptibility to IR or an IR-related condition. Such conditions include hypertension, dyslipidaemia, type 2 diabetes, obesity or coronary artery disease. The methods are also useful in screening for agents useful in the treatment of these disorders. The present sequence represents an IRM cDNA which is specifically claimed for use in the method of the invention. Note: The present sequence is not shown in the specification, but was obtained from GenBank using the accession number listed in Table 1 (page 25-33).

Db	Sequence	3224	BP;	820	A;	812	C;	769	G;	823	T;	0	U;	0	Other;
Qy	Query Match	36.4%		Score	540.8		DB	7		Length	3224				
Db	Best Local Similarity	69.1%		Pred. No.	4e-139										
Qy	Matches	772;	Conservative	0;	Mismatches	337;	Indels	9;	Gaps	2;					
Db															
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Search completed: June 26, 2004, 21:12:27

JOB TIME : 4/3 SEC

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2004, 20:03:31 ; Search time 4048 Seconds
 (without alignments)
 15900.298 Million cell updates/sec

Title: US-10-667-442-1

Perfect score: 1485

Sequence: 1 ccatggaggcgaaaccttca.....taaaaaaaaaaaaaaaa 1485

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_p1:*
9: gb_pr:*
10: gb_ro:*
11: gb_stb:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
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22: em_ov:*
23: em_pat:*
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25: em_p1:*
26: em_ro:*
27: em_stb:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

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score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match	Length	DB ID	Description
	1	1485	100.0	1485	6 AR265353	Sequence AR265353 Sequence
	2	1485	100.0	1485	6 AR432044	Sequence AR432044 Sequence
	3	1228.6	82.7	1281	6 AX320934	Sequence AX320934 Sequence
	4	1188.2	80.0	1594	6 AX207388	Sequence AX207388 Sequence
	5	1188.2	80.0	1594	6 AX766348	Sequence AX766348 Sequence
	6	1186.2	79.9	1191	6 AR393903	Sequence AR393903 Sequence
	7	1186.2	79.9	1191	6 AX303185	Sequence AX303185 Sequence
	8	1184.6	79.8	1191	6 AX320936	Sequence AX320936 Sequence
	9	1162.6	78.3	1675	6 AR393904	Sequence AR393904 Sequence
	10	1162.6	78.3	1675	6 AX303187	Sequence AX303187 Sequence
	11	1160.6	78.2	1224	6 AR393902	Sequence AR393902 Sequence
	12	1160.6	78.2	1224	6 AX303183	Sequence AX303183 Sequence
	13	1029.4	69.3	2063	6 AX833107	Sequence AX833107 Sequence
	14	1029.4	69.3	2063	9 AK094580	Homo sapi
	15	831.2	56.0	981	6 AX166513	Sequence AX166513 Sequence
	16	792.4	53.4	4973	10 BC055002	Mus muscu
	17	656.2	44.2	711	6 AR393901	Sequence AR393901 Sequence
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	21	556.8	37.5	3367	10 BC058412	Mus muscu
	22	556.8	37.5	3367	10 BC052404	Mus muscu
	23	556.8	37.5	3449	10 BC056396	Mus muscu
	24	553.6	37.3	2045	10 MMTU250940	Sequence AJ250840 Mus muscu
	25	540.8	36.4	3224	6 AX056360	Sequence AJ056360 Sequence
	26	540.8	36.4	3224	9 HSA250839	Homo sapi
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	28	516.4	34.8	3244	6 AX376504	Sequence AX376504 Sequence
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	30	494.4	33.3	2184	10 BC026457	Mus muscu
	31	494.4	33.3	2201	10 AB041542	Mus muscu
	32	481.6	32.4	1257	6 AR411704	Sequence AR411704 Sequence
	33	481.6	32.4	1826	6 AR411703	Sequence AR411703 Sequence
	34	481.6	32.4	2143	9 AY098866	Homo sapi
	35	480	32.3	1487	6 AX504245	Sequence AX504245 Sequence
	36	480	32.3	1858	9 BC015792	Homo sapi
	37	476.2	32.1	1787	6 AX056359	Sequence AX056359 Sequence
	38	469.6	31.6	827	9 BC021666	Homo sapi
	39	468.4	31.5	2028	9 BC045760	Homo sapi
	40	466.8	31.4	1864	6 AX642304	Sequence AX642304 Sequence
	41	462	31.1	1591	6 AX768900	Sequence AX768900 Sequence
	42	458.2	30.9	1640	6 AX179651	Sequence AX179651 Sequence
	43	457.4	30.8	2038	9 AB056389	Macaca fa
	44	445.4	30.0	1868	9 AK057849	Homo sapi
	45	441.8	29.8	2182	6 AX364903	Sequence AX364903 Sequence

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AR265353	AR265353	Sequence 1 from patent US 6492155.	AR265353	AR265353.1	GI:29693863	Unknown.	Unclassified.
						Ye,J., Yan,C., Di Francesco,V. and Beasley,E.M.	1 (bases 1 to 1485)
						Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof	
						Patent: US 6492155-A 1 10-DEC-2002;	JOURNAL

Pred. No. is the number of results predicted by chance to have a

FEATURES source	Location/Qualifiers
1. .1485	Score 1485; DB 6; Length 1485;
/organism="unknown"	
/mol_type="genomic DNA"	
ORIGIN	
Query Match	100.0%; score 1485; DB 6; Length 1485;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1485;	Mismatches 0; Indels 0; Gaps 0;
Db	
Qy	1 CCATGGGAGCCAACTTCAGAGCATGTCTTCAAGAGCACCTTGACTCTGTCCAGAAGGAGTTCA 1080
Db	1 CGGATTCTTCTCAGACATGTCTTCAAGAGCACCTTGACTCTGTCCAGAAGGAGTTCA 1080
Qy	1 TAATTTCACAGAGAAAAAGTAACAGGAGACTTTAACAAAAGACAACCAAATCTAGCCT 1140
Db	1 TAATTTCACAGAGAAAAAGTAACAGGAGACTTTAACAAAAGACAACCAAATCTAGCCT 1140
Qy	1 TGGAAACAAACCAAGGACCCAAAGGTGAGGATGGTCTGCATTG 1200
Db	1 TGGAAACAAACCAAGGACCCAAAGGTGAGGATGGTCTGCATTG 1200
Qy	1 ATGTCTCTTCTTCTGGACAATCTCATGCCAACTCTCATGTCAGAAAGAAAG 1260
Db	1 ATGTCTCTTCTTCTGGACAATCTCATGCCAACTCTCATGTCAGAAAG 1260
Qy	1 CTGACAGTAGCTCTGCCACTCCACACACCAGTGAATATATT 1320
Db	1 CTGACAGTAGCTCTGCCACTCCACACACCAGTGAATATATT 1320
Qy	1 CAAAAAGGAGGACACACAGTGAAGGGCTCTGGCTGAGCTTCATTTC 1380
Db	1 CAAAAAGGAGGACACACAGTGAAGGGCTCTGGCTGAGCTTCATTTC 1380
Qy	1 ACATCAATCAACTGTCGATCTAGGAAAGTCACTTAGCCACTTCTGTGCTTTACTTTA 1440
Db	1 ACATCAATCAACTGTCGATCTAGGAAAGTCACTTAGCCACTTCTGTGCTTTACTTTA 1440
Qy	1 TTTATCTAAATGAGAGGGTTATACTAAAAAA 1485
Db	1 TTTATCTAAATGAGAGGGTTATACTAAAAAA 1485
Qy	RESULT 2
Db	AR432044 Locus AR432044
Qy	DEFINITION Sequence 1 from patent US 6653117.
Db	ACCESSION AR432044
Qy	VERSION AR432044.1 GI:40194241
Db	KEYWORDS Unknown.
Qy	ORGANISM Unclassified.
Db	REFERENCE 1 (bases 1 to 1485) AUTHORS Ye,J., Yan,C., Di Francesco,V. and Beasley,E.M. TITLE Isolated human kinase Proteins JOURNAL Patent: US 6653117-A 1 25-NOV-2003; FEATURES Location/Qualifiers Source 1. .1485 /organism="unknown" /mol_type="genomic DNA"
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Qy	1 TTGACCACTTGAATTTGGGAGCTTGGGGAGGTCTGGCAATTG 1200
Db	1 CCATGGGAGCGAACACTTCAGGAAACCCAGCTTGGGGAGGTCTGGCAATTG 1200
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Db	61 ATATGAATGATATAACTGGGATGCACTTCAAGAACGGAAACTTCCGT 840
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Db	781 TACTCGAACCTAACCGAACCTAACCGTCACTTCAAGAACGGAAACTTCCGT 900
Qy	721 CGACTGTGTAACCTACCGAACCTAACCGTCACTTCAAGAACGGAAACTTCCGT 780
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Qy	781 ATATGAATGATATAACTGGGATGCACTTCAAGAACGGAAACTTCCGT 900
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Qy	901 CTAATAAAGGCAAGGATGATCTACCTTGAACCTGAGGAATTGGAGT 960
Db	901 CTAATAAAGGCAAGGATGATCTACCTTGAACCTGAGGAATTGGAGT 960
Qy	121 TACAGAGAAATGATACCAAGAAGATGTGGCAATGAGATGGAGT 180
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Qy	181	TGGAGGGCAATGAAGTGAGAAATGTCTCAAGGAACTCCAGATCATGCAGGGTCTGGAGC	240	Qy	1261	CTGACAGTAGCTCCTGCCACTCACACACCATGACTTAGAAAAATGTGAATATAATT	1320
Db	181	TGGAGGGCAATGAAGTGAGAAATGTCTCAAGGAACTCCAGATCATGCAGGGTCTGGAGC	240	Db	1261	CTGACAGTAGCTCCTGCCACTCACACACCATGACTTAGAAAAATGTGAATATAATT	1320
Qy	241	ACCCCTTCCTGGTTAATTGGTGGTATTCTTCCAGATGAGAACATGTTCATGGGG	300	Qy	1321	CAAAAAAGGGCAGCAACACAGTGAAAGGGCTCTGGAAAGAAGTCATTTC	1380
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Qy	301	TGGACTCTCTGGGGAGCCTGGAGACCTTCCAGATGAGAACATTTCAAGG	360	Qy	1381	ACATCAATCAACTGTGTGATCTAGGCAAGTCAGTGTGCTTACTTTA	1440
Db	301	TGGACTCTCTGGGGAGCCTGGAGACCTTCCAGATGAGAACATTTCAAGG	360	Db	1381	ACATCAATCAACTGTGTGATCTAGGCAAGTCAGTGTGCTTACTTTA	1440
Qy	361	AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCACTTGAGAACACC	420	Qy	1441	TTTATCTAAAATGAGAGGGTTACTAAAAAA	1485
Db	361	AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCACTTGAGAACACC	420	Db	1441	TTTATCTAAAATGAGAGGGTTACTAAAAAA	1485
Qy	421	AGCGCATTCAGGATATGAAAGCTGACAATATTACTTGAGAACATGGGACG	480	RESULT 3			
Db	421	AGCGCATTCAGGATATGAAAGCTGACAATATTACTTGAGAACATGGGACG	480	AX320934	1281 bp	DNA	linear
Qy	481	TGCACATCACAGATTCAACATTGCTGGATGCTGCCAGGGACACAGATTACCA	540	DEFINITION	Sequence 1 from Patent WO0181589.	PAT 14-DEC-2001	
Db	481	TGCACATCACAGATTCAACATTGCTGGATGCTGCCAGGGACACAGATTACCA	540	ACCESSION	AX320934		
Qy	541	TGGCTGGCACCAAGCTTACATGGCACCTGAGATGTTCAAGTCCAGAAAGGAGGAGCT	600	VERSION	AX320934.1		
Db	541	TGGCTGGCACCAAGCTTACATGGCACCTGAGATGTTCAAGTCCAGAAAGGAGGAGCT	600	KEYWORDS	GI:17902480		
Qy	601	ATTCCTTTGCTGACTGGTGCCTGGAGTCAGGGCATATGAACTGCTGAGGGCC	660	SOURCE	Homo sapiens (human)		
Db	601	ATTCCTTTGCTGACTGGTGCCTGGAGTCAGGGCATATGAACTGCTGAGGGCC	660	ORGANISM	Homo sapiens		
Qy	661	GGAGACCGTATCATATTGCTCCAGTACTTCAGCAGGAAATTGTACACAGTTGAGA	720	REFERENCE	1. Meyers, R. and Hunter, J.J.		
Db	661	GGAGACCGTATCATATTGCTCCAGTACTTCAGCAGGAAATTGTACACAGTTGAGA	720	AUTHORS	14911 novel protein kinases and uses therefor		
Qy	721	CGACTGTTGTAACCTACCCATTCCAGACCAAGGATTCTCAGTTATCTGATGTCCAGA	780	TITLE	Patent: WO 0181589-A-1 01-NOV-2001;		
Db	721	CGACTGTTGTAACCTACCCATTCCAGACCAAGGATTCTCAGTTATCTGATGTCCAGA	780	JOURNAL	Millennium Pharmaceuticals, Inc. (US)		
Qy	781	TACTCGAACCTTAATCCAGACCAAGGATTCTCAGTTATCTGATGTCCAGA	840	FEATURES	Location/Qualifiers		
Db	781	TACTCGAACCTTAATCCAGACCAAGGATTCTCAGTTATCTGATGTCCAGA	840	Source	1. 1281		
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Qy	1021	GGGATTTCTCTCGACATGTCTTCAGCAAGGACCTTGACTCTGTCCAGAAGGACTCA	1080	LLGGDLRHYLQNVHFKBETVLFICELVMALDYLQNRIIHRDMKPDNLILLEHGHV			
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Qy	1321	ACATCAATCAACTGTGTGATCTAGGCAAGACAGTGTGCTTACTTTA	1440	Qy	61 TTGACCACTTTGAAATTTCAGGCAATTGGGAGGTCTGCAATT	120	
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DEFINITION	Sequence 1 from Patent WO0155356.				
ACCESSION	AX207388				
VERSION	AX207388.1 GI:15395198				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
ORGANISM	Homo sapiens Human protein kinases and protein kinase-like enzymes				
REFERENCE	Plowman, G., Whyte, D., Manning, G., Sudarsanam, S. and Martinez, R. Human protein kinases and protein kinase-like enzymes Patent: WO 0155356-A 1 02-AUG-2001; Sugen, Inc. (US)				
AUTHORS	Plowman, G., Whyte, D., Manning, G., Sudarsanam, S. and Martinez, R. Human protein kinases and protein kinase-like enzymes Patent: WO 0155356-A 1 02-AUG-2001; Sugen, Inc. (US)				
TITLE	Human protein kinases and protein kinase-like enzymes				
JOURNAL	Patent: WO 0155356-A 1 02-AUG-2001;				
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Db	Query Match 80.0%; Score 1188.2; DB 6; Length 1594; Best Local Similarity 99.7%; Pred. No. 2.7e-286; Matches 1190; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
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Qy	2.41 ACCCTTCTGGTTAATTGGCTCCAGTGGGATGGAGACATGGTGTGG 3.00 2.87 ACCCTTCTGGTTAATTGGCTCCAGTGGGATGGAGACATGGTGTGG 3.46				
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Qy	3.61 AAGAACAGTGAAGCTTCAATGGGAGACATGGTGTGG 4.20 4.07 AAGAACAGTGAAGCTTCAATGGTGTGG 4.66				
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Db	Query Match 80.0%; Score 1188.2; DB 6; Length 1594; Best Local Similarity 99.7%; Pred. No. 2.7e-286; Matches 1190; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
Qy	5.41 TGGCTGGCACAAAGCCTTACATGGCACCTGCTCAGCTCCAGTTG 5.87 TGGCTGGCACAAAGCCTTACATGGCACCTGCTCAGCTCCAGTTG Qy 601 ATTCCTTGTGACTGGTGTGACTGGCTCCCTGGAGTGTGCTGGCATATG 646 647 ATTCCTTGTGACTGGTGTGACTGGCTCCCTGGAGTGTGCTGGCATATG Qy 661 GGAGACCGTATCATATTCGCTCCAGTACTGGCTCCAGTACTCTAAAGC 720 707 GGAGACCGTATCATATTCGCTCCAGTACTGGCTCCAGTACTCTAAAGC Qy 721 CGACTGTGTAACTTACCCCTTCAGCTGGCTCACAGGAATTTGTA 780 781 TACTCGAACCTAATCCAGAACCGATTTCAGTTCTGGTGTCACTTCTAAAGC 826 767 CGACTGTGTAACTTACCCCTTCAGCTGGCTCACAGGAATTTGTA Qy 827 TACTCGAACCTAATCCAGAACCGATTTCAGTTCTGGTGTCACTTCTAAAGC 840 841 ATATGAATGATAACCGAACCGATTTCAGCTGGCTCACAGGAATTTGTA 900 901 CTAATAAAGGCAAGCTAACATGGGATGGCTGAACTTCCGGT 946 947 CTAATAAAGGCAAGCTAACATGGGATGGCTGAACTTCCGGT Qy 961 CCAAACCTCTACATAAGAAAAAGGCTCTGGCAAAAGAAGGAACTTCA 1002 1007 CCAAACCTCTACATAAGAAAAAGGCTCTGGCAAAAGAAGGAACTTCA 1021 1021 GCGATTCTCTCAAGACATGGTCTTCAAGAGGCCCTGACTCTGGTCC 1067 1067 GCGATTCTCTCAAGACATGGTCTTCAAGAGGCCCTGACTCTGGTCC 1081 1081 TAATTTTCAACAGAGAAAAGTAACAGGGACTTTAACAAAGACA 1127 1127 TAATTTTCAACAGAGAAAAGTAACAGGGACTTTAACAAAGACA 1140 1140 TAATTTTCAACAGAGAAAAGTAACAGGGACTTTAACAAAGACA 1186 1186 TAATTTTCAACAGAGAAAAGTAACAGGGACTTTAACAAAGACA 1200 1201 ATGTCTTCTCTCAAGACATCTCATGCCAGAAC 1235 1247 1247 ATGTCTTCTCTGGGACAATCTCATGCCAGAAC 1281				
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 VERSION AR393903.1 GI:40121079
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1191)
 AUTHORS Hu, Y.; Nepomnyichy, B.; Wang, X. and Donoho, G.
 TITLE Human kinase proteins and polynucleotides encoding the same
 JOURNAL Patent: US 6617147-A 10 09-SEP-2003;
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RESULT 7
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 LOCUS AX303185 1191 bp DNA linear PAT 30-NOV-2001
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 ACCESSION AX303185
 VERSION AX303185.1 GI:17383668
 KEYWORDS SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1. Hu, Y., Nepomnyichy, B., Wang, X., Donoho, G., Scoville, J. and
 Walk, D.W.
 TITLE Human kinase proteins and polytynucleotides encoding the same
 JOURNAL Patent: WO 0181557-A 10 01-NOV-2001;
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ORIGIN Query Match 79.9%; Score 1186.2; DB 6; Length 1191;
 Best Local Similarity 99.7%; Pred. No. 8.4e-286;
 Matches 1188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 3 ATGGGAGCCAAACACTTCAAGAAAACCAACCGTGTGATGAAAATGAACGATGTCAACTTT 62
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		KEYWORDS	Homo sapiens (human)
		SOURCE	Homo sapiens
		ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens
REFERENCE	AUTHORS	Meyers, R. and Hunter, J.J.	14911 novel protein kinase molecules and uses therefor
	TITLE	14911 novel protein kinase molecules and uses therefor	
JOURNAL	PATENT	WO 0181589-A 3 01-NOV-2001; Millennium Pharmaceuticals, Inc. (US)	
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LOCUS		DEFINITION Sequence 12 from patent US 6617147.			Qy	781	TACTGAACTTAATCCAGACCAACGATTTCCTCAGTTATCTGATGTCCAGAACCTCCCGT	840
ACCESSION		ACCESSION AR393904			Db	1191	TACTGAACTTAATCCAGACCAACGATTTCCTCAGTTATCTGATGTCCAGAACCTCCCGT	1250
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FEATURES		FEATURES			Qy	961	CCAAACACTCTACATAAGAAAAGCGTCTGGCAAGAACAGGAGGATATGAGGAAT	1020
REFERENCE		REFERENCE 1 (bases 1 to 1675)			Db	1371	CCAAACACTCTACATAAGAAAAGCGTCTGGCAAGAACAGGAGGATATGAGGAAT	1430
AUTHORS		AUTHORS Hu, Y., Nepomnichy, B., Wang, X. and Donoho, G.			Qy	1021	CGCGATTCTCTCAGACATGTCTCTTCAGACAGGACCTTGACTCTGTCAGGAGGTCA	1080
TITLE		TITLE Human kinase proteins and polynucleotides encoding the same			Db	1431	CGCGATTCTCTCAGACATGTCTCTTCAGACAGGACCTTGACTCTGTCAGGAGGTCA	1490
JOURNAL		JOURNAL Patent: US 6617147-A 12-09-SEP-2003;			Qy	1081	TAATTTCAACAGAGAAAAGTAAACAGGAGACTTTAACAAATCTAGCCT	1140
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source		source 1..1675 /organism="unknown" /mol_type="genomic DNA"			Qy	1141	TGGAACAAACCAAGGCCACAAAGGTGAGGATGGTCAGAATAACA	1185
ORIGIN		ORIGIN			Db	1551	TGGAACAAACCAAGGCCACAAAGTGAATTCAGGCAATGGGAAAGGCTGATTG	1595
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Best Local Similarity		Best Local Similarity 98.8%; Pred. No. 6.9e-280;			AX303187			
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Qy	61	TTGACCACTTGAATTTCGGAGCCATTGGAAAGGCCATTGGAGCTCTGCATTG	120		VERSION AX303187			
Db	471	TTGACCACTTGAATTTCGGAGCCATTGGAAAGGCCATTGGAGCTCTGCATTG	530		KEYWORDS			
Qy	121	TACAGAAGAATGATAACCAAGAGATGTGGCAATGAAGTACATGAATAACAGAGT	180		SOURCE Homo sapiens (human)			
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Qy	181	TGGAGGCCAATGAAGTGAAGAACCTGGCTTCAAGAACCTGGCTCTGGAGC	240		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
Db	591	TGGAGGCCAATGAAGAACCTGGCTTCAAGAACCTGGCTCTGGAGC	650		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
Qy	241	ACCCCTTCTGGTTAATTGTGGTATTCCTCCAAAGATGAGGAAGACATGTGG	300					
Db	651	ACCCCTTCTGGTTAATTGTGGTATTCCTCCAAAGATGAGGAAGACATGTGG	710					

REFERENCE	Hu, Y., Nepomnichy, B., Wang, X., Donoho, G., Scoville, J. and Walk, D.W.	Scoville, J. and Walk, D.W.
AUTHORS	Human kinase Proteins and Polynucleotides encoding the same	
TITLE	Patent: WO 0181557-A 12 01-NOV-2001; Lexicon Genetics Incorporated (US)	
JOURNAL	Location/Qualifiers	
FEATURES	1. .1675 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon: 9606"	
Source		
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	Query Match Score 1162.6; DB 6; Length 1675; Best Local Similarity 98.8%; Pred. No. 6.9e-280; Matches 1171; Conservative 0; Mismatches 14; Indels 0; Gaps 0;	
Db	1 CCATGGAGCGAACACTCAAGAAACCAACAGTGTGATGAAATGAAGATGTCAACT 60 411 CCATGGAGCCAACCTCAAGAAACCAACAGTGTGATGAAATGAAGATGTCAACT 470	
Qy	61 TTGACCACTTTGAAATTTCGGAGCCATTGGAAAGGCAGTTGGGGAGGTCTGCATTG 120 471 TTGACCACTTTGAAATTTCGGAGCCATTGGAAAGGCAGTGTGGAAAGGTCTGCATTG 530	
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Qy	181 TGGAGGCCAATGAAAGTGGAAATTGTCTTCAGGAAACTCCAGATCATGCAAGGCTCTGGAGC 240 591 TGGAGGCCAATGAAAGTGGAAATTGTCTTCAGGAAACTCCAGATCATGCAAGGCTCTGGAGC 650	
Db	241 ACCCTTCCTGGTTAATTGTGGTATTCCCTCCAAGATGAGGAAGACATGTTCATGGTGG 300 651 ACCCTTCCTGGTTAATTGTGGTATTCCCTCCAAGATGAGGAAGACATGTTCATGGTGG 710	
Qy	301 TGGACCTCCTGCTGGGTGGAGACCTGGTTATCACCTGCAAGAACAGTCCACTTCAGG 360 711 TGGACCTCCTGCTGGGTGGAGACCTGGTTATCACCTGCAACAGAACGTCCACTTCAGG 770	
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Qy	421 AGGGCATTCATTCAACAGGGATATGAGGCTGACAATATTTCAGCTGAGAACATGGGCACG 480 831 AGGGCATTCATTCAACAGGGATATGAGGCTGACAATATTTCAGCTGAGAACATGGGCACG 890	
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Db	901	AATAAAGCCAGGCTGAATTGTGATCCTACCTTGGAGTC	960	Qy	361	AAGAAACAGTGAAGCTCTTCATCTGTGAGCTGGTCATGCCCTGACTACCTGCAAGAAC	420
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Db	1081	ATTTCAACAGAGAAAAGTAACAGGGACTTTAACAGGAAACCAATCTAGCCTTG	1140	Qy	541	TGGCTGGGACCAAGGCTTACATGGCACCCTGAGATGTTCAAGTCCAGAAAGGAGGGCT	600
Qy	1143	GAACAAACAAAGACCCACAAAGGTGAGGTGAGTGGTCAGAAATAACA	1185	Db	872	TGGCTGGGACCAAGGCTTACATGGCACCCTGAGATGTTCAAGTCCAGAAAGGAGGGCT	931
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Qy	661	GGAGACCGTATCATATTGCTCAGTACTCCAGCAAGGAATTGTCACACAGTTGAGA	720	Qy	721	CGACTGTGTAACTTACCCCTCTGCCTGGTCACAGGAATGGTGTCACTTCTTAAAGC	780
Db	992	GGAGACCGTATCATATTGCTCAGTACTCCAGCAAGGAATTGTCACACAGTTGAGA	1051	Db	1052	CGACTGTGTAACTTACCCCTCTGCCTGGTCACAGGAATGGTGTCACTTCTTAAAGC	1111
Qy	721	CGACTGTGTAACTTACCCCTCTGCCTGGTCACAGGAATGGTGTCACTTCTTAAAGC	1111	Db	1112	TACTCGAACCTTACCCCTCTGCCTGGTCACAGGAATGGTGTCACTTCTTAAAGC	1171
Qy	781	TACTCGAACCTTACCCCTCTGCCTGGTCACAGGAATGGTGTCACTTCTTAAAGC	840	Qy	841	ATATGAATGATAAACTGGGATGCGATTTCAGAAGGAGGTCACTTCAGAACCTCCGGT	900
Db	1112	TACTCGAACCTTACCCCTCTGCCTGGTCACAGGAATGGTGTCACTTCTTAAAGC	1171	Db	1172	ATATGAATGATAAACTGGGATGCGATTTCAGAAGGAGGTCACTTCAGAACCTCCGGT	1231
Qy	901	CTAATAAAGGCAGGCTGAAATTGTGATCCTACCTTGAACCTTGGAGT	960	Qy	961	CCAAACCTCTACATAAGAAAAAGCGTCTGGCAAAGGAAGGGAGATATGGAAAT	1020
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ACCESSION	AX833107			VERSION	GI:39919242		linear
KEYWORDS				SOURCE	Homo sapiens (human)		PRI 15-JUL-2002
ORGANISM				ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		clone BRAMY2010464, moderately
REFERENCE				REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		similar to Mus musculus mRNA for serine/threonine protein kinase.
AUTHORS				AUTHORS	Isozai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshihikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.		AK094580
TITLE				TITLE	Full-length cDNA sequences		AK094580.1
JOURNAL				JOURNAL	Patent: EP 1347046-A 231 24-SEP-2003; Research Association for Biotechnology (JP)		GI:21753667
FEATURES				FEATURES	Location/Qualifiers		oligo capping; fis (full insert sequence).
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ORIGIN				ORIGIN			Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE				REFERENCE			1
AUTHORS				AUTHORS	Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyma, T., Irie, R., Otsubuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Nakamura, Y., Kikuchi, H., Matsuoka, M., Murakawa, K., Kanehori, K., Yamashita, H., Wagatsuma, M., Sugiyama, A., Kawakami, B., Suzuki, Y., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.		
ACCESSION				ACCESSION	NEDO human cDNA sequencing project		
VERSION				VERSION	Unpublished		
KEYWORDS				KEYWORDS			
ORGANISM				ORGANISM			
REFERENCE				REFERENCE			
AUTHORS				AUTHORS			

REFERENCE 2 (bases 1 to 2063)
 AUTHORS Isogai, T. and Yamamoto, J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI team); 2-6-7
 Kazusa-Kamata, Kisaizaru, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' - & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES source
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ORIGIN

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 VERSION AX166513.1 GI:14546858
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,
 Planagan, P. and Clary, D.S.
 TITLE Novel human protein kinases and protein kinase-like enzymes
 JOURNAL Patent: WO 0138503-A 4 31-MAY-2001;
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 Qy 483 CACATCACAGATTCAACATTGCTGCGATGCTGCCAGGGAGAACAGATTACCAACATG 542
 Db 481 CACATCACAGATTCAACATTGCTGCGATGCTGCCAGGGAGAACAGATTACCAACATG 540
 Qy 543 GCTGGACCAAGCCTTACATGGCACCTGAGATGTTCAAGTCCAGAAAAGGAGGGCTAT 602
 Db 541 GCTGGACCAAGCCTTACATGGCACCTGAGATGTTCAAGTCCAGAAAAGGAGGGCTAT 600
 Qy 603 TCCTTGCTGACTTCACTTACCCCTGCCTGGAGTGACGGCATATGAACTGCTGAGGCCGG 662
 Db 601 TCCTTGCTGACTTACCCCTGCCTGGAGTGACGGCATATGAACTGCTGAGGCCGG 660
 Qy 663 AGACCGTATCATATTGCTCAGTACTTACCCCTGCCTGGAGTGACGGCATATGAACTGCTGAGGCCGG 722
 Db 661 AGACCGTATCATATTGCTCAGTACTTACCCCTGCCTGGAGTGACGGCATATGAACTGCTGAGGCCGG 720
 Qy 723 ACTGTGTGTAATTGCTCAGTACTTACCCCTGCCTGGAGTGACGGCATATGAACTGCTGAGGCCGG 782
 Db 721 ACTGTGTGTAATTGCTCAGTACTTACCCCTGCCTGGAGTGACGGCATATGAACTGCTGAGGCCGG 780
 Qy 783 CTCGAACCTAATTGCAACGATTTCAGTGTCACTTCAAGTGTCCAGAACTTCCGGTAT 842
 Db 781 AGAAGGAAGACTGGCATGTC-----CAAACGAAGTAACAAAAGGAAGCAGG 825
 Qy 843 ATGAATGATAAAACTGGGATGCAATTTCAGAAGGGCTCAATTCCAGGTTCAATTCT 902
 Db 826 CTCTCTGGCTTAAGTTAGTAGTTAGTATAACCAATTGGGACACCAACTGTCCTCCTTG 885
 Qy 903 AATAAAGGCAGGTGAATTGTGATCCTACCTTGAACTTGAGGAATGATTGGAGTCC 962
 Db 886 CAGAAAGGCAGGTGAATTGTGATCCTACCTTGAACTTGAGGAATGATTGGAGTCC 945
 Qy 963 AAAACCTCTACATAAGAAAAAAAGCGTCTGGCAAAG 998
 Db 946 AAAACCTCTACATAAGAAAAAAAGCGTCTGGCAAAG 981

Search completed: June 26, 2004, 22:20:15
 Job time : 4053 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:47:04 ; Search time 44 Seconds
 (without alignments)
 2839.664 Million cell updates/sec

Title: US-10-667-442-2

Perfect score: 2104

Sequence: 1 MGANTSRKPPVFDENEDVNPF.....NLALEQTQDPQGEDGQNNNL 396

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp Rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp Unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Q96wj8 blumeria gr 17 675 32.1 3 Q96wj8
 Q8i4w3 plasmodium 18 548.5 26.1 5 Q8i4w3
 Q43380 avena sativ 19 521 24.8 10 Q43380
 Q8myf1 dictyosteli 20 516 24.5 456 5 Q8myf1
 Q9txb8 dictyosteli 21 515.5 24.5 648 5 Q9txb8
 Q8lfc1 arabidopsis 22 514.5 24.5 465 10 Q8lfc1
 Q25115 hemicentrot 23 513.5 24.4 352 5 Q25115
 Q9y777 metarhizium 24 512.5 24.4 522 3 Q9y777
 Q97116 amblyomma a 25 512 24.3 462 5 Q97116
 26 508.5 24.2 421 5 Q97115
 27 508 24.1 371 5 Q97114
 28 507.5 24.1 530 3 Q42793
 29 507.5 24.1 919 3 Q8nik8
 Q8nik8 emericella 30 507 24.1 352 5 Q16957
 aplysis cal 31 506.5 24.1 772 5 Q18846
 caenorhabdi 32 506.5 24.1 917 3 Q9hgb0
 botrytis ci 33 504.5 24.0 536 3 Q9p466
 neurospora 34 502.5 23.9 502 3 Q8j129
 35 501.5 23.8 726 4 Q7z327
 36 501.5 23.8 726 6 Q7yql2
 37 501.5 23.8 726 6 Q7yql1
 38 501.5 23.8 758 6 Q9bb29
 39 501 23.8 360 5 Q16933
 ancylostoma 40 500.5 23.8 351 13 Q9own3
 xenopus lae 41 500.5 23.8 490 3 Q96um3
 42 500.5 23.8 733 4 Q96j38
 homo sapien 43 499.5 23.7 587 4 Q8ww06
 44 498.5 23.7 343 6 Q9mzd8
 ovis aries 45 498.5 23.7 539 3 Q01143
 magnaporthe

ALIGNMENTS

RESULT 1

Q8bgw6 ID Q8bgw6
 AC Q8bgw6;
 PRELIMINARY; DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DE Similar to A930015B13R1K. DE 25, Last annotation update.
 GN Mus musculus (Mouse). RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; RA "Analysis of the mouse transcriptome based on functional annotation of
 OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. RT 60,770 full-length cDNAs.";
 OC NCBI_TaxID=10090; RN [1] RT SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
 RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002). DR EMBL: AK036266; BAC29366.1;
 DR EMBL: AK04474; BAC31941.1; DR MGI:2442403; A930015B13Rik.
 DR GO:005524; F:ATP binding; DR GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO:0004713; F:protein tyrosine kinase activity; IEA.
 DR GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase. DR InterPro; IPR002290; Ser-thr_pk kinase.
 DR InterPro; IPR008271; Ser-thr_pkin_AS. DR InterPro; IPR001245; Tyr_pk kinase.
 DR Pfam; PF00069; Pkinase; 1. DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1. DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TYRKc; 1.
 DR Q9vn23 drosophila

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1899	90.3	398	11	Q8bgw6	Q8bgw6 mus musculu	
2	1726	82.0	368	11	Q7tpq4	Q7tpq4 mus musculu	
3	1438.5	68.4	414	11	Q7tmd3	Q7tmd3 mus musculu	
4	1437.5	68.3	414	11	Q9jjx8	Q9jjx8 mus musculu	
5	1434.5	68.2	414	11	Q8c4eo	Q8c4eo mus musculu	
6	1425.5	67.8	414	4	Q9ny57	Q9ny57 homo sapien	
7	1421.5	67.6	414	4	Q8iy14	Q8iy14 homo sapien	
8	1324	62.9	486	4	Q86ux6	Q86ux6 homo sapien	
9	1317.5	62.6	488	11	Q9jjg4	Q9jjg4 mus musculu	
10	1317.5	62.6	488	11	Q8ozv4	Q8ozv4 mus musculu	
11	1137.5	54.1	369	4	Q96ba3	Q96ba3 homo sapien	
12	1137.5	54.1	369	4	Q86ue1	Q86ue1 homo sapien	
13	1122.5	53.4	368	6	Q9bgt4	Q9bgt4 macaca fasc	
14	843.5	40.1	379	5	Q21483	Q21483 caenorhabdi	
15	822	39.1	166	4	Q8ww08	Q8ww08 homo sapien	
16	711.5	33.8	700	5	Q9vn23	Q9vn23 drosophila	

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 SQ SEQUENCE; 398 AA; 46509 MW; 689BCA5B25CF18BB CRC64;

Query Match 90.3%; Score 1899; DB 11; Length 398;
 Best Local Similarity 89.7%; Pred. No. 2.5e-150;
 Matches 357; Conservative 22; Mismatches 17; Indels 2; Gaps 1;

Qy	1 MGANTTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIIVQRNDTKKMCAMCKMNKQKCV 60	Query Match 82.0%; Score 1726; DB 11; Length 368;
Db	1 MGANTSSKAPVFDENEDVNFDHFEILRAIGKGSFGEVCIIVQRNDTKKMCAMCKMNKQKCV 60	Best Local Similarity 82.9%; Pred. No. 6.6e-136;
Qy	61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDDMFMVVQLLGGDLRYHLQONVHFKE 120	Mismatches 19; Indels 32; Gaps 2;
Db	61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDDMFMVVQLLGGDLRYHLQONVHFKE 120	KW Hypothetical protein.
Qy	121 ETVKLFICELVMAVDLYLQNLQRIIHRDMKPDNLLDEHGHVHTIDFNIAAMLPRETQITM 180	SQ SEQUENCE 368 AA; 43213 MW; 0DB7F6977C39BB56 CRC64;
Db	121 DTVKLPICELVALADLYLQNLQRIIHRDMKPDNLLDEHGHVHTIDFNIAMLPKETRITV 180	Query Match 82.0%; Score 1726; DB 11; Length 368;
Qy	181 AGTKPYMAPEMFSSRKAGGYSFAVDWWSLGVTAYELLGRGRRPYHRSSTSSEKEIVHTFET 240	Best Local Similarity 82.9%; Pred. No. 6.6e-136;
Db	181 AGTKPYMAPEMFTSRKETGYSFAVDWWSLGVTAYELLGRGRRPYHRSSTSSEKEIVHTFET 240	Matches 330; Conservative 19; Mismatches 17; Indels 32; Gaps 2;
Qy	241 TVVTPYSAWSQEMVSLLKKLLEPNPQDFQSQLDQNPYMMNDINWDAYQKRLLIPGFIP 300	Query Match 82.0%; Score 1726; DB 11; Length 368;
Db	241 AIVTPYSAWSQEMVSLLKKLLEPNPQDFQSHLTIDIQNFPMISDMNWDAYQKRLLIPGFIP 300	Best Local Similarity 82.9%; Pred. No. 6.6e-136;
Qy	301 NKGRLNCDPTFELEMILESKPLHKKKRKLAKKEKDMRKCDSSQTCLLQEHDLSVQKEFI 360	Mismatches 19; Indels 32; Gaps 2;
Db	301 TKGRLNCDPTFELEMILESKPLHKKKRKLAKKEKEMKCSDDSSQTCLLQEHDLSVQKEFI 360	KW Hypothetical protein.
Qy	361 IFNREKVNRDNFKQPNLALEQTKD - PQGEDQNNNL 396	Query Match 82.0%; Score 1726; DB 11; Length 368;
Db	361 IFNREKVKSDFNQRQANLALEQTKNNTTEEEEDQNNNL 398	Best Local Similarity 82.9%; Pred. No. 6.6e-136;
RESULT 2		Matches 330; Conservative 19; Mismatches 17; Indels 32; Gaps 2;
Q7TPQ4	PRELIMINARY; PRT; 368 AA.	Query Match 82.0%; Score 1726; DB 11; Length 368;
ID Q7TP04	PRELIMINARY; PRT; 368 AA.	Best Local Similarity 82.9%; Pred. No. 6.6e-136;
AC Q7TPQ4	PRELIMINARY; PRT; 368 AA.	Mismatches 19; Indels 32; Gaps 2;
DT 01-OCT-2003	(TREMBLrel. 25, Created)	KW Hypothetical protein.
DT 01-OCT-2003	(TREMBLrel. 25, Last sequence update)	SEQUENCE FROM N.A.
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)	TISSUE=Olfactory epithelium; MEDLINE=22388257; PubMed=12477932;
DE Hypothetical protein.	OS Mus musculus (Mouse)	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.
OS Mus musculus (Mouse)	OC	OC
OC	OC	OC
OC	OC	OC
NCBI_TaxID=10090;	NCBI_TaxID=10090;	NCBI_TaxID=10090;
RN [1]	RN	RN
RP	RP	RP
SEQUENCE FROM N.A.		SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium; MEDLINE=22388257; PubMed=12477932;		STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,		RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,		RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,		RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,		RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,		RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human		RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";		RT and mouse cDNA sequences.";
RT		RT

RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6; TISSUE=Brain;
RC	Strausberg R.;
RA	Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RL	
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6; TISSUE=Brain;
RA	Strausberg R.;
RL	Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC052404; AAH52404.1; -.
DR	EMBL; BC056396; AAH56396.1; -.
KW	Hypothetical protein.
SQ	SEQUENCE 414 AA; 47916 MW; 3C394415790594P3 CRC64;
	Query Match 68.4%; Score 1438.5; DB 11; Length 414;
	Best Local Similarity 68.5%; Pred. No. 8.1e-112;
	Matches 280; Conservative 39; Mismatches 71; Indels 19; Gaps 1
Qy	1 MGANTSRKPPVFDENEDVNFDHFELRAIGKGSFCEVCIVQANDTKMCMAMCKYMKQKCV 6
Db	1 MGGNHSHKPPVFDENEVNFDHFQILRAIGKGSFCKVCIWQKRDTKTYAMKCYMKQKCV 6
Qy	61 ERNEVRNVFKELQIMQGLEHPFPFLVNLWYSQDDEDMFMVVDLLGGDLRYHLQQNVTQFKE 1
Db	61 ERDEVNVFRELQIMQGLEHPFPFLVNLWYSQDDEDMFMVVDLLGGDLRYHLQQNVTQFTE 1
Qy	121 ETVKLFIGELVMALDYLNQRIIHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 1
Db	121 GTVVKLYICELALALEYLQRYHIIFRDIKPDNILLDEHGHVHTDFNIAATVLKGSBKASSM 1
Qy	181 AGTKPKYMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLOWLRGRPYHRSSTSKEIVHTP 2
Db	181 AGTKPKYMAPEVFQVYVDPGGSYPVDDWWSLGVTAYELLOWLRGRPYEIHSAATPIDEILNMFP 2
Qy	239 ETVVVTVPSAWSQEMVSLLKKLLEPNPQRFSQLSDVQNFPMNDINWDAYFQKRLIPGF 2
Db	241 KVERVHYSSSTWCEGMVSLKKLLTKDPESSLRDIQSMTYLADMMNWDAYFEKALMPGF 3
Qy	299 IPNKGRLNCDPTPELEEMILESPLHKCKCKRLLAK--KEKDMRKCDSSQTCILQEHLDSVQK 3
Db	301 VPKNGRNLNCPTPELEEMILESPLHKCKCKRLLAKRSRSDSTKDSCLPQNGHQOCLETVRK 3
Qy	358 EPIIFNRKEVNRDFNKQPNLALEQTKDPQG-----EDGQNNVNL 396
Db	361 EPIIFNRKEKRRQQGHN-----GQLSDLGRIGSQTSSKLQDGRNNNI 403
	RESULT 4
RN	SEQUENCE FROM N.A.
RP	MEDLINE=20164328; PubMed=10700184;
RX	Ruiz-Perez V.L., Ide S.B., Strom T.M., Lorenz B., Wilson D., Woods K., King L., Francomano C., Freisinger P., Spranger S., Marino B., Dallapiccola B., Wright M., Meitinger T., Polymeropoulos M.H., [1]

RT "Mutations in a new gene in Ellis-van creveld syndrome and Weyers acrodermal dysostosis."; RL Nat. Genet. 24: 283-286 (2000). CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. DR EMBL; AJ250840; CAB76566.1; -. DR HSSP; P05132; 1CTP. DR MGD; MGI:1927552; Stk32: DR GO; GO:0005524; F:ATP binding; IEA. DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA. DR GO; GO:0016740; F:transferase activity; IEA. DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA. DR InterPro; IPR000719; Prot kinase. DR InterPro; IPR002290; Ser_Thr_pk kinase. DR InterPro; IPR008271; Ser_Thr_pkin_AS. DR Pfam; PF00069; Pkinase; 1. DR ProDom; PD000001; Prot kinase; 1. DR SMART; SM00220; S_TKC; 1. DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1. KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase. SQ SEQUENCE 414 AA; 47917 MW; BE394415790B9A13 CRC64;					
Query Match 68.3%; Score 1437.5; DB 11; Length 414; Best Local Similarity 69.7%; Pred. No. 9.8e-112; Matches 278; Conservative 38; Missmatches 64; Indels 19; Gap 1					
Qy 1 MGANTSRKPPVDEDENEDVNFDHPEIILRAIGKGSFGEVTCIVQKNDTKRMCAAMKYMNKKQ	Db 1 MGGNTHSHKPPVFPDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKRMCAAMKYMNKKQ				
Qy 61 ERNEVRNVFKBLQIMQGLEHPFLVNLWYSFQDDEEDMFMVVDDLLGGDLRYHLQQNVH	Db 61 ERDEVNVFRELQIMQGLEHPFLVNLWYSFQDDEEDMFMVVDDLLGGDLRYHLQQNVH				
Qy 121 ETVKLPICELVMALDYLQNQRRIHRDMKPDNMILLDEGHVHITDFNIAAMLPRETQI	Db 121 GTRVKLYICBLALALEYLQRYHIIHRDIKPDMNILLDEGHVHITDFNIAATVLKGSBKA				
Qy 181 AGTKPYMAEMFS--SRKGAGYSFAVDWWISLGVTAYELLRGRRPYHIRSSTSKEIVV	Db 181 AGTKPYMAPEVFQVTVGDGGPGYSYPVDWWISLGVTAYELLRGWRPYEHSATPIDELIL				
Qy 239 ETTVVVTYPSAWSQEMVSLLKKLEPPNPDQRFSQLSDVQNFPMNDINWDAVFQKRLLI	Db 241 KVVERVHYSSSTWCCEGMVSSLKKLLTKDPESRLLRDIQSMTYLADMNWDADFEKALM				
Qy 299 IPNKGRLLNCDPTFELEEMILESKPLHKKKCRRLAK-KERDMRKCDSQSQTCLLQQEHLDS	Db 301 VPKNGRLLNCDPTFELEEMILESKPLHKKKCRRLAKHRSRDSTKDCPVLNGHLQQCLET				
Qy 358 EPIIFNREKVNRFNKRQPNLALBQTQKDPOGEDGQNNNL 396	Db 361 EPIIFNREKLRQQ-----QGHDGQLSDL 383				
RESULT 5					
Q8C4E0 ID Q8C4E0 PRELIMINARY ; PRT; 414 AA.	AC Q8C4E0;				
Q8C4E0 AC Q8C4E0;	DT 01-MAR-2003 (TREMBLrel. 23, Created)				
Q8C4E0 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
Q8C4E0 DE Serine threonine kinase 32.	DE Serine threonine kinase 32.				
GN STK32.	GN STK32.				
OS Mus musculus (Mouse)	OS Mus musculus (Mouse)				
OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX NCBI_TaxID=10090;	OX NCBI_TaxID=10090;				
RN [1]	RN [1]				
RP SEQUENCE FROM N.A.	RP SEQUENCE=C57BL/6J; TISSUE=Cerebellum;				
RC	RC				

RX	The FANTOM Consortium,	RX	MEDLINE=20164328; PubMed=10700184;
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;	RA	Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,
RA	"Analysis of the mouse transcriptome based on functional annotation of	RA	King L., Francomano C., Freisinger P., Spranger S., Marino B.,
RT	60,770 full-length cDNAs.;"	RA	Dallapiccola B., Wright M., Meitinger T., Polymeropoulos M.H.,
RT	Nature 420:563-573 (2002).	RA	Goodship J.;
RL	EMBL; AR082468; BAC38500.1; -.	RT	"Mutations in a new gene in Ellis-van Creveld syndrome and Weyers
DR	MGD; MGI:1927552; Stk32.	RT	acrodermal dysostosis."
DR	GO; GO:0005524; F:ATP binding; IEA.	RL	Nat. Genet. 24:283-286 (2000).
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.	CC	-1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.	CC	DR EMBL; AJ250839; CAB76471.1; -.
DR	GO; GO:0006468; F:protein amino acid phosphorylation; IEA.	DR	DR HSSP; P05132; 1CTP.
DR	InterPro; IPR000719; Prot_kinase.	DR	DR GO; GO:0005524; F:ATP binding; IEA.
DR	InterPro; IPR002290; Ser_Chr_pk kinase.	DR	DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR	InterPro; IPR008271; Ser_thr_pkin_AS.	DR	DR GO; GO:0016740; F:transferase activity; IEA.
DR	InterPro; IPR001245; Tyr_pk kinase.	DR	DR InterPro; IPR000719; Prot kinase.
DR	Pfam; PF00069; pk kinase; 1.	DR	DR InterPro; IPR002290; Ser_thr_pk kinase.
DR	ProDom; PD000001; Prot_kinase; 1.	DR	DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR	SMART; SM00220; S_TKC; 1.	DR	DR Pfam; PF00069; pk kinase; 1.
DR	SMART; SM00219; TyrKC; 1.	DR	DR ProDom; PD000001; Prot_kinase; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	DR	DR SMART; SM00220; S_TKC; 1.
DR	PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.	DR	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	DR	DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
SQ	SEQUENCE 414 AA; 47884 MW; 9C394364BE19E945 CRC64;	DR	DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Query Match	68.2%; Score 1434.5; DB 11; Length 414;	KW	KW ATP-binding; Kinase; Serine/threonine-protein kinase; transferase.
Best Local Similarity	68.2%; Pred. No. 1.7e-111; Gaps 4;	SQ	SQ SEQUENCE 414 AA; 47883 MW; 8PCDS8A67EP09B08 CRC64;
Matches 279; Conservative 40; Mismatches 71; Indels 19; Gaps 4;	Query Match	67.8%; Score 1425.5; DB 4; Length 414;	
QY	1 MGANTSRKPPVFDENEDVNFDHFBIIRAIKGKGSFGBVCIVQKNDTKKMCAAMKYMNNQKCV 60	Best Local Similarity	68.2%; Pred. No. 9.9e-111; Gaps 3;
DB	1 MGCHSHSHKPPVFDENEEVNFDFQIIRAIKGKGSFGKVCIVQKRDTKKMYAMKYMNNQKCV 60	Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;	
QY	61 ERNEVRNVFPELQLQIMOGLEHPLFLVNLWYSFQDEEDMFMVVDLQLGGDLRYHLQQNTHFKS 120	QY	1 MGANTSRKPPVFDENEDVNFDHFBIIRAIKGKGSFGBVCIVQKNDTKKMCAAMKYMNNQKCV 60
DB	61 ERDEVNRNVFRELQIMOGLEHPLFLVNLWYSFQDEEDMFMVVDLQLGGDLRYHLQQNTHFKS 120	DB	1 MGGNHSHKPPVFDENEEVNFDFQIIRAIKGKGSFGKVCIVQKRDTKKMYAMKYMNNQKCV 60
QY	121 ETVKLFICBLVMDYLNQNORIIHRDMKPDNILLDEHGHVHITDENIAAMLPRETQITTM 180	QY	61 ERNEVRNVFPELQLQIMOGLEHPLFLVNLWYSFQDEEDMFMVVDLQLGGDLRYHLQQNTHFKS 120
DB	121 GTVKLYICELLALEYLQRYHIHRDIKPDNILLDEHGHVHITDENIAMLPRETQITTM 180	DB	61 ERDEVNRNVFRELQIMOGLEHPLFLVNLWYSFQDEEDMFMVVDLQLGGDLRYHLQQNTHFKS 120
QY	181 AGRKPKYMAPEMFS--SRKGAGGYSFAVDWWSLGVTAYELLRGRRPYHRSSTSQQKIVHTF 238	QY	121 ETVKLFICBLVMDYLNQNORIIHRDMKPDNILLDEHGHVHITDENIAAMLPRETQITTM 180
DB	181 AGRKPKYMAPEMFS--SRKGAGGYSFAVDWWSLGVTAYELLRGRRPYHRSSTSQQKIVHTF 238	DB	121 GTVKLYICELLALEYLQRYHIHRDIKPDNILLDEHGHVHITDENIAAMLPRETQITTM 180
QY	239 ETYYVTTYPSAWSQEMVSLKLKLEPNPDRFSQLSDVQNFPYMDINWDAVFKRLLIPGF 298	QY	181 AGRKPKYMAPEMFS--SRKGAGGYSFAVDWWSLGVTAYELLRGRRPYHRSSTSQQKIVHTF 238
DB	241 KVVERVHYSSSTWCEGMVSLKLKLTQDPESRVSSHLDIQSVPLADMNWDAVFKALMPGF 300	DB	181 AGRKPKYMAPEMFS--SRKGAGGYSFAVDWWSLGVTAYELLRGRRPYHRSSTSQQKIVHTF 238
QY	299 IPNKGRNLNCDFTPLEBEMILESKPLHKKKKRLLAK-KEKDMRKKCDSSQTCLLQEHLDVQK 357	QY	239 ETYYVTTYPSAWSQEMVSLKLKLEPNPDRFSQLSDVQNFPYMDINWDAVFKRLLIPGF 298
DB	301 VPNGKGRNLNCDFTPLEBEMILESKPLHKKKKRLLAK-HRSRSDSTKDCSPLNGHLQHQCLETVRK 360	DB	241 KVVERVHYSSSTWCEGMVALLRKCLLTQDPESRVSSHLDIQSVPLADMNWDAVFKALMPGF 300
QY	358 EPILFNREKVNDRFNKRQPNLALEQTKDPOG-----EDGQNNNL 396	QY	299 IPNKGRNLNCDFTPLEBEMILESKPLHKKKKRLLAK-KEKDMRKKCDSSQTCLLQEHLDVQK 357
DB	361 EPITFNREKLRQQGHN-----GQLSDLGRIGSQTSKQQLQDGRRNNNI 403	DB	301 VPNGKGRNLNCDFTPLEBEMILESKPLHKKKKRLLAK-HRSRSDSTKDCSPLNGHLQHQCLETVRK 360
RESULT 6	Q9NY57 PRELIMINARY; PRT; 414 AA.	RESULT 7	Q8IY14 PRELIMINARY; PRT; 414 AA.
ID	Q9NY57	ID	Q8IY14
AC	Q9NY57;	AC	Q8IY14
DT	01-OCT-2000 (TREMBLrel. 15, Created)	DT	01-MAR-2003 (TREMBLrel. 23, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE	Serine/threonine protein kinase.	DE	Serine/threonine protein kinase.
OS	Homo sapiens (Human).	OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxID	[1]	NCBI_TaxID	9606;
RN	SEQUENCE FROM N.A.	RN	[1]
RP	TISSUE=Brain;	RP	NCBI_TaxID=9606;
RC		RC	

"Isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AB041542; BAA95027.1; -.
HSSP; P05132; 1CTP.
DR MGD; MGI:2385336; Pke.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPRO00719; Prot kinase.
DR InterPro; IPRO002290; Ser_Thr_Pkinase.
DR InterPro; IPRO008271; Ser_thr_Pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 488 AA; 55276 MW; 310483FF69E24E39 CRC64;
Query Match 62.6%; Score 1317.5; DB 11; Length 488;
Best Local Similarity 64.3%; Pred. No. 1.3e-101;
Matches 250; Conservative 54; Mismatches 76; Indels 9; Gaps 6
Qy SRKPPVFDENEDVNFDHFEIILRAIGKGSFGEVCTIVQKNDTKKMCAMKYMNNQKCVERNE
Db 77 SARRPVFDDKEDVNFDHFQILRAIGKGSFGKVCIQKRDTEKMYAMKYMNNQQCIERDE
Qy 66 RNVFKEELQIMQGLEHPFLVNLWYSFQDDEEDMFMVVVDLLGGDLRYHLQQNVHFKEEETVY
Db 137 RNVFRELEIILQBIEHVPLVNLWYSFQDDEEDMFMVVVDLLGGDLRYHLQQNVQFSEDTVFTV
Qy 126 FICELVMALDYLQNQRRIIHRDMKPDNILLDEIGHVHITDFNIAAMLPRETQITMAGTH
Db 197 YMAMEIYLRSQHIIHRDVVKPDNILLDEQGH AHLTDFNIAТИIKDGERATALAGTH
Qy 186 YMAMEFSS--RKGAGYSFAVDWWSLGVTAELLRRGRPYHIRSSTSSKEIVHTFETTY
Db 257 YMAMEIFHSFVNGGTGYSFEVDWWSVGMMAYELLRGWRPYDIHSSNAVESLVQLFSTVS
Qy 244 TYPSSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMDINWDAVFQKRLIPGFIPNIV
Db 317 QYVPTWSKEMVALLRKLLTVNPEHRFSSLQDMQTAPS LAHVLDLSEKKVPEPGFVVPNT
Qy 304 RLNCDPTELEEMILES KPLHKCKCRKLA KKEKDMDRKCDSSQT--CLLQEQHLDSSVQKEF
Db 377 RLHCDPTELEEMILES RPLHKCKCRKLA KNEKS RDSSQSENDYLQDCDAIQQDFET
Qy 362 FNREKVN RDENK ROPNL ALEGQT KDPQGED 390
Db 437 FNREKL-----KRSQELMSEPPP GPETSD 460
RESULT 10
Q8QZV4 PRELIMINARY; PRT; 488 AA.
ID Q8QZV4 AC Q8QZV4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical serine/threonine protein kinase.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

OX	NCBI_TaxID=9606;	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKerrian K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Straubberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC	-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	RA	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., DR
DR	EMBL; BC015792; AAH15792.1; -.	RA	DR
DR	GO: GO:0005524; F:ATP binding; IEA.	RA	DR
DR	GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.	RA	DR
DR	GO: GO:0016740; F:transferase activity; IEA.	RA	DR
DR	GO: GO:0006468; P:protein amino acid phosphorylation; IEA.	RA	DR
DR	InterPro; IPR000719; Prot_kinase.	RA	DR
DR	InterPro; IPR008271; Ser_Thr_pkkin_AS.	RA	DR
DR	PFam; PF00069; pkincase; 1.	RP	SEQUENCE FROM N.A.
DR	ProDom; PD000001; Prot_kinase; 1.	RC	TISSUE=Testis;
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	RA	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR	PROSITE; PS500108; PROTEIN_KINASE_ST; 1.	RL	DR
KW	Hypothetical protein; ATP-binding; Kinase;	DR	GO: GO:0005524; F:ATP binding; IEA.
KW	Serine/threonine-protein kinase; Transferase.	DR	GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
SQ	SEQUENCE 369 AA; 42425 MW; 83C54C4AF7D792E5 CRC64;	DR	GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
Query	54.1%; Score 1137.5; DB 4; Length 369; Best Local Similarity 62.8%; Pred. No. 9.9e-87; Matches 218; Conservative 47; Mismatches 73; Indels 9; Gaps 3;	DR	InterPro; IPR000719; Prot_kinase.
Db	48 MCAMKYMNNKQKCVERNVYRNFKELQIMQGLEHPLFLVNLWYSFQDEEDMFMVVDLLGGD 107 1 MYAMKYMNNKQQCITERDEVNVFRELEIQLQEIEHVFLVNLWYSFQDEEDMFMVVDLLGGD 60	DR	InterPro; IPR001245; Tyr_pk kinase.
Query	108 LRYHLQQNVHFKKEETVKLPFICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNI 167	DR	InterPro; IPR000290; Ser_Thr_pk kinase.
Db	61 LRYHLQQNVQFQSEDTVRLYICEMALADYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120	DR	InterPro; IPR0008271; Ser_Thr_pk kinase.
Query	168 AAMLPRETQITTMAGTKPKYMAPEMFSS--RKGAGGYSAFDWWSLGLVTAYBLRGRRPYHI 225	DR	SMART; SM00220; S_TKC; 1.
Db	121 ATIKDGERATALAGTKPKYMAPAEIPHSFVNNGGTGYSFEVDWWSVGMDAYELLRGWRPYDI 180	DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Query	226 RSSTSSKBEVHTVTPSAWSQEMVSLLKLLPEQPNPDSQVQNFPMYNDIN 285	DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Db	181 HSSNAVESLVLQPLSTVSVQVVPWSKEMVALLRKLLTVNPBEHRLSSLQDVAAPALAGVL 240	DR	SEQUENCE 369 AA; 42395 MW; B152C66BB2D786B4 CRC64;
Query	286 WDAVFQKRLIPGFTIPNKGRLNCDPTFEELLEMILESKPLHKKKRCLAKKEKDMRKCDSSQT 345	QY	Query Match 54.1%; Score 1137.5; DB 4; Length 369; Best Local Similarity 62.8%; Pred. No. 9.9e-87; Matches 218; Conservative 47; Mismatches 73; Indels 9; Gaps 3;
Db	241 WDHLSEKRVEPGFPVNKGRLHCDPTFELBEMILESRPLHKKKRCLAKNKSRDNSSQS 300	QY	1 MYAMKYMNNKQQCITERDEVNVFRELEIQLQEIEHVFLVNLWYSFQDEEDMFMVVDLLGGD 60
Query	346 -CLIQEHLDVSQKEFIIIFNREKVNRDFTNKRQPNLAEQTKDQPGED 390	DB	108 LRYHLQQNVHFKKEETVKLPFICELVMALDYLQHQHIIHRDVKPDNILLDERGHAHLTDFNI 167
Db	301 ENDYLQDCLDIAIQQDFVIFNREKL----KRSQDLPREPLPAPESRD 342	QY	61 LRYHLQQNVQFSEDTVRLYICEMALADYLRLGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
RESULT 12	Q86UE1 PRELIMINARY; PRT; 369 AA.	QY	120 AAMILPRETQITTMAGTKPKYMAPEMFSS--RKGAGGYSAFDWWSLGLVTAYBLRGRRPYHI 225
ID	Q86UE1 PRELIMINARY; PRT; 369 AA.	DB	121 ATIKDGERATALAGTKPKYMAPAEIPHSFVNNGGTGYSFEVDWWSVGMDAYELLRGWRPYDI 180
AC	Q86UE1	QY	1226 RSSTSSKBEVHTVTPSAWSQEMVSLLKLLPEQPNPDSQVQNFPMYNDIN 285
DT	01-JUN-2003 (TREMBLrel. 24, Created)	DB	181 HSSNAVESLVLQPLSTVSVQVVPWSKEMVALLRKLLTVNPBEHRLSSLQDVAAPALAGVL 240
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)	QY	186 WDAVFQKRLIPGFTIPNKGRLNCDPTFEELLEMILESKPLHKKKRCLAKKEKDMRKCDSSQT 345
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DB	241 WDHLSEKRVEPGFPVNKGRLHCDPTFELBEMILESRPLHKKKRCLAKNKSRDNSSQS 300
DE	PKE protein.	QY	246 -CLIQEHLDVSQKEFIIIFNREKVNRDFTNKRQPNLAEQTKDQPGED 390
OS	Homo sapiens (Human).	DB	301 ENDYLQDCLDIAIQQDFVIFNREKL----KRSQDLPREPLPAPESRD 342
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	QY	346 -CLIQEHLDVSQKEFIIIFNREKVNRDFTNKRQPNLAEQTKDQPGED 390
OC	NCBI_TaxID=9606;	DB	301 ENDYLQDCLDIAIQQDFVIFNREKL----KRSQDLPREPLPAPESRD 342
RN	SEQUENCE FROM N.A.	RESULT 13	Hypothetical protein.
RC	TISSUE=Testis;	Q9BGT4	RESULT 13
RX	MEDLINE=22388257; PubMed=12477932;	ID Q9BGT4	PRELIMINARY;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Bhat N.K., Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,	AC Q9BGT4;	PRT; 368 AA.
RA	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.	DT 01-JUN-2001 (TrEMBLrel. 17, Created)	
RA	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."	DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
RA	[1]	DR	

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9541;

[1] SEQUENCE FROM N.A.

RC TISSUE=Frontal cortex;

RA Osada N.; Hida M.; Kusuda J.; Tanuma R.; Iseki K.; Hirai M.; Terao K.,

RA Suzuki Y.; Sugano S.; Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain cDNA libraries.";

RT Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; AB056389; BAB33045.1; -.

DR GO; GO:0005524; P:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

KW PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 368 AA; 42218 MW; 5D7269B32DABCC14 CRC64;

Query Match Score 1122.5; DB 6; Length 368;

Best Local Similarity 62.8%; Pred. No. 1.8e-85;

Matches 218; Conservative 44; Mismatches 76; Indels 9; Gaps 3;

Db 48 MCAMKYMNKQKCVERNVNFKEIPLQIMQGLEHPPFLVNLWYSFQDEEDMFMVVDLLGGD 107

Db 1 MYAMKYMNKQQCIEDEVNVFRELGIQLQIEHVPLVNLWYSFQDEEDMFMVVDLLGGD 60

Qy 108 LRYHLQQNIVHEKEBTVKLFICELVMALDYLQNLQNQRITHDMKPDNTILLDEEHGHVHTDFNI 167

Db 61 LRYHLQQNIVQFSEDTVRVLYICEMALADYLCLCGOHIIRHDVKPDNTILLDERGH AHLTDFN 120

Qy 168 AAMLPRETQITTMAGTKPYPMAPEMFS--RKGAGYSFAVDWWSLGVTAYELLGRRRPYHI 225

Db 121 ATIRKDGERATALAGTKPYPMAPEIFHSFVNNGGTGYSFEBDWWSLGVMAYELLRGWRPYDI 180

Qy 226 RSSTSSKKEIVHTFETTVTVTYPSSAWSQEMVSLLKQKLEPNPDRQFSQLSDVQNFPMYNDIN 285

Db 181 HSSNAVESLVLQQLPTSTVSVQYVPTWSREMVALRKLLTVNPEHRFSSLQDVQAAPALAGVL 240

Qy 286 WDAVQKRLIPGFIPNKGRNLCDPTFELEMILLESPLHKKKKRLLAKKEKDMRKCDSSQT 345

Db 241 WGHLSKEKRVEPDPVPKGRHLCDPTFELEMILLESPLHKKKKRLLAKNKSRDNSRDSSQS 300

Qy 346 --CLLQEHLDSVQKKEPIIIFPNREKVNRFDPNKRQPNLALEQTKDPOQGED 390

Db 301 ENDYIQLQDCCLDAIQQDFVIFTNREKL----KRSQDLPEPLAPEPRD 342

Qy 320 SKPLHKKKKKRLLAKKEKDMRKCDSSQTCLQEHLDSVQKKEPIIIFPNREKVNRFDPNKRQPN 377

Db 327 STPIH--RRRTNHNNNSGRSSSEPBONNALVE---VSKAFIDFSRHNV---KIBPN 373

RESULT 14

Q21483 ID Q21483 PRELIMINARY; PRT; 379 AA.

AC Q21483 PRELIMINARY; PRT; 379 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE M03C11.1 protein.

GN Caenorhabditis elegans.

OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Peloderrinae; Caenorhabditis.

NCBI_TaxID=6239;

[1] SEQUENCE FROM N.A.

RA McMurray A.A.; Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.

RL [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=9069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode *C.elegans*: A platform for investigating biology.";

RT Science 282:2012-2018 (1998).

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; Z49128; CAA88953.1; -.

DR PIR; T23688; T23688.

DR HSSP; Q63450; LA06.

DR WormPep; M03C11.1; CB03492.

DR GO; GO:0005524; P:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 379 AA; 43632 MW; 5E2090A15812D27D CRC64;

Query Match Score 40.1%; Score 843.5; DB 5; Length 379;

Best Local Similarity 44.1%; Pred. No. 3.8e-62;

Mismatches 70; Mismatches 117; Indels 13; Gaps 4;

Matches 158; Conservative 218; Gaps 15;

Qy 22 HFEILRAIGKGSFGESVCIQKNDTKKMCAMKYMNKQKCVERNBVRNVPFKSLQIMQGLBLHP 81

Db 27 HPSVIRSTIGRAFGKVKCIVQERKTKYPAALKYMNTRKRCITERGVAAANVIRETLTLLSKMSHP 86

Qy 82 FLYNLWYSPQDDBEDOMFMVVDLLGGDLRVLHQNLQVNVPFKSETVKLPICBLWALDYLQNQR 141

Db 87 FIVNLWYTQDGDWYMYVSDLLGGDWYHLSQDQGAHLLTDLNLATQLEDQDLATSYSGTRPYPMAPEIYATYLEIEDG 206

Qy 142 I1HRDMPDNILLDEGHVHITDFNIAAMLPRETQITTMAGTKPYPMAPEMFS--RKGAG 199

Db 147 IVARDIKPENILLBQGHAHLLTDLNLATQLEDQDLATSYSGTRPYPMAPEIYATYLEIEDG 207

Qy 200 YSFAVDWWSLGVTYAYELLGRGRPYHIRSSTSKEIVHTPETTVTYPSSAWSQEMVSLLKK 259

Db 207 YDSRVDDWWALGVCTYEMLRGRTPPFESSRTKPEEAYVAFRESSIPIYPAHWPTDLIQFINS 266

Qy 260 LLEPNPNDQRFSQLSDVQNFPYMDNDINTWDVQKRLIPGFIPNKGRNLNCDFPTFELEMILE 319

Db 267 MLKFDFKBRKLVLGLEAIKKHSYTERIDPKSVFEKKPSVPIPCKEGLNCDPMYEELEERILY 326

Qy 320 SKPLHKKKKKRLLAKKEKDMRKCDSSQTCLQEHLDSVQKKEPIIIFPNREKVNRFDPNKRQPN 377

Db 327 STPIH--RRRTNHNNNSGRSSSEPBONNALVE---VSKAFIDFSRHNV---KIBPN 373

RESULT 15

QBWU08 ID QBWU08 PRELIMINARY;

AC QBWU08 PRELIMINARY;

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Similar to Serine/threonine kinase 32.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1] SEQUENCE FROM N.A.

RP RP

RC TISSUE=Urinary bladder;
 RA Straubberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTRIN KINASES.
 EMBL; EC021666; AAH21666.1;
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 InterPro; IPR000719; Prot_kinase.
 InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR Pfam; PF00069; pkinase; 1.
 DR PRODom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 166 AA; 19792 MW; CDCF94B54C793BA4 CRC64;

Query Match 39.1%; Score 822; DB 4; Length 166;
 Best Local Similarity 98.7%; Pred. No. 8e-61;
 Matches 155; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKOMCAMKYMNKQOKCV 60
Db	1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKOMAMKYMNKQOKCV 60
Qy	61 ERNEVRNVPKELQIMQGLEHPPFLVNLWYSFQDEEDMFMVVVDLLLGCDLRYHLQQNVHFKE 120
Db	61 ERNEVRNVPKELQIMQGLEHPPFLVNLWYSFQDEEDMFMVVVDLLGGDRLRYHLQQNVHFKE 120
Qy	121 ETVKLPICELVMALDYLQNQRIIHDMKPDNILLDEH 157
Db	121 ETVKLPICELVMALDYLQNQRIIHDMKPDNILLDEH 157

Search completed: June 25, 2004, 10:51:07
 Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:43:09 ; Search time 18 Seconds
 (without alignments)
 1145.543 Million cell updates/sec

Title: US-10-667-442-2
 Perfect score: 2104
 Sequence: 1 MGANTSRKPPVFDENEDVNF.....NLAEQTQDPOGEDQNNL 396

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582.5	27.7	444	1 KRAC DICDI	P54644 dictyosteli
2	537.7	25.5	479	1 PK2 DICDI	P28178 dictyosteli
3	528.5	25.1	648	1 KAPC DICDI	P34099 dictyosteli
4	519	24.7	471	1 KP19_ARATH	Q39030 arabidopsis
5	516.5	24.5	465	1 KP1_KRATH	P42818 arabidopsis
6	513	24.4	680	1 YPK1_YEAST	P12688 saccharomyces
7	511.5	24.3	696	1 SCK1_SCHPO	P50530 schizosacch
8	510.5	24.3	352	1 KAPC_DROME	P12370 drosophila
9	503	23.9	404	1 KAPC_CAEBL	P21137 caenorhabdi
10	502.5	23.9	350	1 KAPA_CRIGR	P25321 cricetulus
11	502.5	23.9	350	1 KAPA_PIG	P36887 sus scrofa
12	502.5	23.9	823	1 SCH9_YEAST	P11792 saccharomyces
13	501.5	23.8	740	1 K6A3_HUMAN	P51812 homo sapien
14	501.5	23.8	740	1 K6A3_MOUSE	P18654 mus musculus
15	501	23.8	677	1 YPK2_YEAST	P18961 saccharomyces
16	500.5	23.8	350	1 KAPG_HUMAN	P22612 homo sapien
17	500.5	23.8	733	1 K6A2_HUMAN	Q15349 homo sapien
18	498.5	23.7	349	1 KAPA_CANFA	Q8mj44 canis familiaris
19	498.5	23.7	350	1 KAPA_HUMAN	P17612 homo sapien
20	498.5	23.7	350	1 KAPA RAT	P27791 rattus norvegicus
21	498.5	23.7	350	1 KAPA_SHEEP	P25098 homo sapien
22	498.5	23.7	689	1 ARK1_HUMAN	P00517 bos taurus
23	496.5	23.6	350	1 KAPA_BOVIN	Q9wut3 m ribosomal protein S6
24	496.5	23.6	733	1 K6A2_MOUSE	P05206 mus musculus
25	496	23.6	350	1 KAPB_MOUSE	Q62074 mus musculus
26	495.5	23.6	586	1 KPCI_MOUSE	P41743 homo sapien
27	495.5	23.6	587	1 KPCI_HUMAN	P18652 gallus gallus
28	494.5	23.5	752	1 K6A1_CHICK	P05986 baccharomyces
29	493.5	23.5	398	1 KAPC_YEAST	Q10364 schizosaccharomyces pombe
30	493.5	23.5	646	1 KDBE_SCHPO	P21146 bos taurus
31	493.5	23.5	689	1 ARK1_BOVIN	Q64682 mesocricetus auratus
32	493	23.4	689	1 ARK1_MESAU	P05132 mus musculus
33	492.5	23.4	350	1 KAPA_MOUSE	

ALIGNMENTS

RESULT 1
 KRAC DICDI
 ID KRAC DICDI STANDARD; PRT; 444 AA.

AC P54644;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DB RAC-family serine/threonine kinase homolog (EC 2.7.1.-).
 GN PKBA OR DAGA.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

RX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX3;
 RA Moon B., Haribabu B., Rabino M., Ortiz B., Reichel G., Skehel P., Williams J.J., Bouzid S., Veron M., Dottin R.P.; Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SBR/THR FAMILY OF PROTEIN KINASES. RAC
 CC -!- SUBFAMILY: STRONGEST TO YEAST YPK1/YPK2.
 CC -!- SIMILARITY: Contains 1 PH domain.

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CC DR EMBL; U15212; AAC76692.1; -.
 DR HSSP; P05132; ICP1P.
 DR DictyBase; DDB003794; pkba.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR InterPro; IPR002290; Ser_Thr_pkinase.
 DR Pfam; PF000433; Pkinase C; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; P800108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; P850011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; P850003; PH DOMAIN; 1.
 DR Transfase; Serine/Threonine-protein kinase; ATP-binding.
 KW DOMAIN 5 100 PH.
 FT DOMAIN 120 374 PROTEIN KINASE.
 FT NP BIND 126 134 ATP (BY SIMILARITY).
 FT BINDING 149 149 ATP (BY SIMILARITY).
 FT ACT SITE 243 243 BY SIMILARITY.
 SQ SEQUNCE 444 AA; 51062 MW; 12367A1A411C5680 CRC64;

RX MEDLINE=93385090; PubMed=8373760;	Qy 127 ICELVMALDYLQNLQRRIHRDMPDNILLDEHGHVHITDFNIAAMLPRETQITTMAGTKPY 186
RA Anjard C., Etchebehere L., Pinaud S., Veron M., Raymond C.D.;	RA "An unusual catalytic subunit for the cAMP-dependent protein kinase of Dictyostelium discoideum";
RT "DDPK3, which plays essential roles during Dictyostelium development, encodes the catalytic subunit of cAMP-dependent protein kinase.";	RT
RL Biochemistry 32:9532-9538 (1993).	RL [3]
RN STRAIN=AX3;	
RC MEDLINE=93066311; PubMed=1332055;	Qy 187 MAPBMPSSRKGAGYSPAYDWISLGVTAYELLRGRRPYHRSSTSKEIVHTPETTVVTP 246
RA Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.;	DB 440 AAEIVLALEFLHKONIVYDLKPENLLIDNQCHIKITDFGFAKRV--EDRTFTLCLGTPY 497
RT "DDPK3, which plays essential roles during Dictyostelium development, encodes the catalytic subunit of cAMP-dependent protein kinase.";	
RT Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705 (1992).	
RL	
CC -!- FUNCTION: Essential for differentiation and fruit morphogenesis.	
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.	
CC -!- SUBUNIT: IN DICTYOSTELIUM THE HOLOENZYME IS A DIMER COMPOSED OF A REGULATOR (R) AND A CATALYTIC (C) SUBUNIT. IN THE PRESENCE OF CAMP IT DISSOCIATES INTO THE ACTIVE C SUBUNIT AND AN R MONOMER.	
CC -!- DEVELOPMENT STAGE: CAPK activity is low in vegetatively growing amoebae, increases during development of aggregation and reaches a maximum at culmination.	
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP subfamily.	
CC	
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CC	
DR EMBL; M38703; -; NOT_ANNOTATED_CDS.	
DR PIR; JQ1150; JQ1150.	
DR HSSP; P05132; IATP.	
DR DictyBase; DDB0003793; pkaC.	
DR InterPro; IPR000961; pkinase C.	
DR InterPro; IPR000719; Prot kinase.	
DR InterPro; IPR0008271; Ser_Thr_pkin_AS.	
DR InterPro; IPR002290; Ser_thr_pkinase.	
DR InterPro; IPR001245; Tyr_pkinase.	
DR Pfam; PF00069; pkinase_1.	
DR Pfam; PF00433; pkinase_C_1.	
DR PRINTS; PR00109; TYRKINASE.	
DR ProDom; PD0000001; Prot_kinase; 1.	
DR SMART; SM00133; S_TK_X_1.	
DR SMART; SM00220; S_TK_G_1.	
DR PROSITE; PS000107; PROTEIN_KINASE_ATP; 1.	
DR PROSITE; PS000108; PROTEIN_KINASE_ST; 1.	
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
KW Transferase; Serine/threonine-protein kinase; ATP-binding; cAMP; Phosphorylation.	
FT DOMAIN 58 64 ASN-RICH.	
FT DOMAIN 136 223 GLN-RICH.	
FT DOMAIN 233 250 THR-RICH.	
FT DOMAIN 336 590 PROTEIN KINASE.	
FT NP BIND 342 350 ATP (BY SIMILARITY).	
FT BINDING 365 365 ATP (BY SIMILARITY).	
FT ACT_SITE 459 459 BY SIMILARITY.	
FT MOD_RES 490 490 PHOSPHORYLATION (BY SIMILARITY).	
SQ SEQUENCEB 648 AA; 74458 MW; D0F9B3A48C58D084 CRC64;	
Query Match 25.1%; Score 528.5; DB 1; Length 648;	
Best Local Similarity 34.2%; Pred. No. 6.e-29; Mismatches 76; Indels 21; Gaps 8;	
Matches 110; Conservative 76; Mismatches 115; Indels 21; Gaps 8;	
Qy 9 PPVFDENEDVNFDPEILRAIGKGSFGEVCIVQKNDTKKMC--AMKYMNKQKCVVERNEVR 66	
DB 325 PPV--NARERIKCBPKQIRVLGTCGKVLIQ--NTKDGCGYYAMKCLNKKAYVQLKQVS 379	
Qy 67 NVPKELOQIMQGLEHPPLVNLWYSPODEEDMFMVVDLLGGDLRYHLQQNWVHFKEETVKLF 126	
DB 380 HLNSEKSILSSIIHHPPFIVNLYQAFQDDEKKYLLEFYAGGEVTHLRKSMKFNSNSTAKFY 439	"Sequence and analysis of chromosome 3 of the plant Arabidopsis

thaliana.";
Nature 408:820-822(2000).

[3]
 SEQUENCE FROM N.A.
 STRAIN=CV. Columbia;

Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
 Palm C.J., Theologis A., Ecker J., Davis R.W.;
 Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

[4]
 SEQUENCE FROM N.A.
 STRAIN=CV. Columbia;

MEDLINE=22954850; PubMed=14593172;
 Yamada K., Lim J.J., Dale J.M., Chen H., Shirn P., Palm C.J.,
 Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 Karlin-Neumann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjali M., Hansen N.F.,
 Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
 Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 "Empirical analysis of transcriptional activity in the *Arabidopsis*
 genome.";

- FUNCTION: May be involved in adaptation of plant to cold or high-salt conditions.
- PTM: Undergoes serine-specific autophosphorylation (By similarity).
- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. 86 kinase subfamily.
- CAUTION: Ref. 4 sequence differs from that shown due to a frameshift in position 391.

BL; D42061; BAA07661.1; -. BL; AC012562; AAG51345.1; -. BL; AP325094; AAK17162.1; -. BL; AY050826; -; NOT_ANNOTATED_CDS. R; S68463; S68463. SP; P05132; 1CTP. InterPro; IPR000961; Pkinase_C. InterPro; IPR000719; Prot_kinase. InterPro; IPR008271; Ser_thr_pkin_AS. InterPro; IPR002290; Ser_thr_pkinase. [am; PF00069; pkinase; 1. [am; PF00433; pkinase_C; 1. eDom; PD000001; Prot_kinase; 1. HART; SM00133; S_TK_X; 1. HART; SM00220; S_TKC; 1. PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

Query	Match	Score	DB	Length
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.				
KW Transferase; Serine/threonine-protein kinase; ATP-binding;				
KW Phosphorylation.				
FT DOMAIN	140	395	PROTEIN_KINASE.	
FT NP BIND	146	154	ATP (BY SIMILARITY).	
FT B ⁻ INDING	169	169	ATP (BY SIMILARITY).	
FT ACT SITE	263	263	BY SIMILARITY.	
FT CONFLICT	250	250	A -> V (IN REF. 1).	
FT CONFLICT	359	360	LS -> VP (IN REF. 1).	
SQ SEQUENCE	471 AA;	53037 MW;	95F007B44B58DFB5 CRC64;	
		24.7%	Score 519; DB 1;	Length 471;

Best Local Similarity 34.0% ; Pred. No. 2e-28;		Matches 108; Conservative 64; Mismatches 122; Indels 24; Gaps 4;	
QY 12 PDENED-----VNFDHFEILRAIGKGSFGEVCIQKNDTKKMCAMKYMNNQK 58		QY 116 PSNDDTDSEKSPPEEVSGVVGIEDFEVLKVVGQAFGKVRQVRLPDKTSEIYAMKVMRKDK 175	
QY 59 CVERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDDEEDMFMVVDLLGGDLRXYHLQQQNVP 118			
Db 176 IVEKNAEXMKAERDILTKIDHPPIVQLKYSFQTQYRLYLVLDPFLNGGHFLPQLYHQGLP 235			
QY 119 KEETVKLFICELVYMLDYLNQNQRRIHDMKPDNJILDEHGHVHITDFNIAAMLPRETOIT 178			
Db 236 REDLARVYTAEIIVSAVSHLHEKGIMHRDLKPENILMDVDGHHVMLTDFGLAKEFEENTRSN 295			
QY 179 TMAGTKPYMAPEMFSSRKAGAGYSPAIVDWWSLGVTAYBLLRGRRPYHRSSTSKEIVHTF 238			
Db 296 SMCGTTBEMAPEIV---RGKGHDKAADWWSVGILLYEMLTGKPPPLGSKGKIQQQKIV--- 349			
QY 239 ETRVVVTYPSAWSQEMVSLLKXLLBPNPDORF----SQLSDVQNFPYMMNDINWDAVFQKRL 294			
Db 350 -KDKIKLQPQFLSNEAHALLKGLLQKEPERRLGSCGPSGABEIKKKHWNFKAINWKCLAREV 408			
QY 295 IPGFIPIPKGRLNCDPTFE 312.			
Db 409 QPSFKPAVSGRQCIANFD 426			
RESULT 5			
KPK1_ARATH ID_KPK1_ARATH	STANDARD;	PRT;	465 AA.
AC P42818;			
DT 01-NOV-1995 (Rel. 32, Created)			
DT 01-NOV-1995 (Rel. 32, Last sequence update)			
DT 15-MAR-2004 (Rel. 43, Last annotation update)			
DE Serine/threonine-protein kinase AtPK1/AtPK6 (EC 2.7.1.-).			
GN ATPK1 OR ATPK6 OR AT3G08730 OR F17O14.20.			
OS Arabidopsis thaliana (Mouse-ear cress).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis;			
OX NCBI_TaxID=3702;			
RN RP SEQUENCE FROM N.A.			
RC STRAIN=CV. Landsberg erecta;			
RX MEDLINE=94292519; PubMed=7912697;			
RA Zhang S.-H., Lawton M.A., Hunter T., Lamb C.J.;			
RT "Atpk1, a novel ribosomal protein kinase gene from Arabidopsis. I.			
RT Isolation, characterization, and expression.";			
RL J. Biol. Chem. 269:17586-17592(1994).			
[1]			
RN RP SEQUENCE FROM N.A.			
RC STRAIN=CV. Columbia;			
RX MEDLINE=95129712; PubMed=7828736;			
RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,			
RA Shinozaki K.;			
RT "Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold or salinity stress in Arabidopsis thaliana.";			
RT FEBS Lett. 358:199-204(1995).			
[2]			
RN RP SEQUENCE FROM N.A.			
RC STRAIN=CV. Columbia;			
RX MEDLINE=21016720; PubMed=11130713;			
RA Salanoubat M., Lemke K., Rieger M., Ansorge W., Unseld M.,			
RA Partmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,			
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,			
RA De Simone V., Choisne N., Artiguenave P., Robert C., Brottier P.,			
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,			
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,			
RA Wurtzbach B., Drzonek H., Erfle H., Jordan N., Bangert S.,			
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,			
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,			
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,			
[3]			

GO; GO:0005829; C:cytosol; IDA.	
GO; GO:0005886; C:plasma membrane; IDA.	
GO; GO:0004674; F:protein serine/threonine kinase activity; IMP.	
GO; GO:0006897; P:endocytosis; IMP.	
GO; GO:0006468; P:protein amino acid phosphorylation; IMP.	
GO; GO:0006655; P:sphingolipid metabolism; IMP.	
InterPro; IPR000961; Pkinase C.	
InterPro; IPR000719; Prot_kinase.	
InterPro; IPR008271; Ser_thr_pkinase.	
InterPro; IPR002290; Ser_thr_pkinase.	
Pfam; PF00069; Pkinase_1.	
Pfam; PF00433; Pkinase_C_1.	
ProDom; PD000001; Prot_kinase; 1.	
SMART; SMM00133; S_TK_X; 1.	
SMART; SMM00220; S_TKC; 1.	
PROSITE; PS000107; PROTEIN_KINASE_ATP; 1.	
PROSITE; PS000108; PROTEIN_KINASE_ST; 1.	
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
Transferase; Serine/threonine-protein kinase; ATP-binding.	
DOMAIN 347 602 PROTEIN_KINASE.	
NP BIND 353 361 ATP (BY SIMILARITY).	
BINDING 376 376 ATP (BY SIMILARITY).	
ACT SITE 470 470 BY SIMILARITY.	
CONFLICT 201 201 P -> L (IN REF. 2).	
CONFLICT 553 553 M -> I (IN REF. 2).	
SEQUENCE 680 AA; 76479 MW; 00112BBBB849CD2B5 CRC64;	
Query Match 24.4%; Score 513; DB 1; Length 680;	
Best Local Similarity 32.0%; Pred. No. 8e-28;	
Mismatches 78; Indels 42; Gaps 10;	
Conservative Matches 115; Conservative 78;	
CC 8 KPPVFDENEDVNFDHFELLRAIGKGSFGEVCIVQKNDTKKMCKAMKYMNKQKCVTERNEVRN 67	
CC 335 KP---SRNPKPLSIDDFDFFLKVIGKGSFGKVMQVRKCDTQKVYALKAIRKSIVSKSEVTH 391	
CC 68 VPKELQIMQGLEHPFLVNLWYSFQDEEDDMFMVVDLILLGGDLIRYHQIQLQQNVHFKETVKLF 127	
CC 392 TLAERTVLAIRDPCPFIVPLKFSFQSPEKLYFVLAFLINGGELFYHLQKEGRFDLSRARPYT 451	
CC 128 CELVMALDYLNQRRIIHDMKPDNILLDEHGHVHTDPNIAAMLPRETQIT-TMAGTKPY 186.	
CC 452 AELLCALDNLHKLDVVYRDLKPENILLDYGQHIALCDFGLCKLNMKDDDKTDTFCGTPEY 511	
CC 187 MAPEMFSSRKGAGYSFAVDWWSLGLYTAYBLLRGRRPYHRSSTSKEIVVHTFETTV---V 243	
CC 512 LAPELL---LGLGYTKAVDWTLGVLLYEMLTGLPPYY-----DEDVPKMYKILQEPL 562	
CC 244 TYPSAWSQEMVSLLKKLLEPNPNDQR--FSQLSDVQNFPYMDNDINWDAVFQKRLIIPGFIPN 301	
CC 563 VFPDGFDRAKDLILLGILSRDPTTRRLGYNGADEIRNHPPFSQLSWKRLLMKGYIPPYKPA 622	
CC 302 KGRLNCDPTFELBEMILESKPLHKKKRKLAKKEKDMDRKCDSSQTCLLQEHL-DSVQKEF 359	
CC 623 VS--NSMDTSNPDEEFFTREKPI-----DS----VVDEYLSESVQKQF 658	
SULT 7	
K1_SCHPO STANDARD; PRT; 696 AA.	
P50530; Q9UTF3; 01-OCT-1996 (Rel. 34, Created)	
16-OCT-2001 (Rel. 40, Last sequence update)	
28-FEB-2003 (Rel. 41, Last annotation update)	
Serine/threonine-protein kinase sck1 (EC 2.7.1.37).	
SCK1 OR SPAC1B9.02C.	
Schizosaccharomyces pombe (Fission yeast).	
Eukaryota; Fungi; Ascomycota; Schizosaccharomyces;	
Schizosaccharomycetales; Schizosaccharomyctaceae;	
NCBI_TaxID=4896;	
[1] SEQUENCE FROM N.A. MEDLINE=96120227; PubMed=7498728;	
SEQUENCE FROM N.A. MEDLINE=21848401; PubMed=11859360;	
SEQUENCE FROM N.A. STRAIN=972;	
RC RX MEDLINE=21848401; PubMed=11859360;	
RA RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Stewart A., Bowman S.,	
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Churcher C.M.,	
RA Brooks K., Brown D., Brown S., Chillingworth T., Fraser A.,	
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Hodson G.,	
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson K.,	
RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,	
RA James K., Jones M., Leather S., McDonald S., McLean J.,	
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,	
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,	
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,	
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,	
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,	
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,	
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,	
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,	
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,	
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,	
RA Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mottier S.,	
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,	
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,	
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,	
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Fornburg S.L.,	
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,	
RT "The genome sequence of Schizosaccharomyces pombe." ;	
RT Nature 415:871-880(2002).	
CC - - CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.	
CC - - SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP	
CC subfamily.	
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CC CC	
CC EMBL; D38108; BAA07286.1; -.	
CC EMBL; AL109951; CAB53053.1; -.	
DR PIR; S55694; S55694.	
DR HSSP; P05132; 1CTP.	
DR Genedb_Spombe; SPAC1B9.02C; -.	
DR InterPro; IPR008973; C2_CalB.	
DR InterPro; IPR000961; Pkinase_C.	
DR InterPro; IPR000719; Prot_kinase.	
DR InterPro; IPR008271; Ser_thr_pkin_AS.	
DR InterPro; IPR002290; Ser_thr_pkinase.	
DR InterPro; IPR001245; Tyr_pkinase.	
DR SMART; SM00239; C2; 1.	
DR SMART; SM00133; S_TK_X; 1.	
DR SMART; SM00220; S_TKC; 1.	
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.	
DR Transferase; Serine/threonine-protein kinase; ATP-binding; CAMP.	
KW DOMAIN 302 563 PROTEIN KINASE.	

NP_BIND 308 316 ATP (BY SIMILARITY).
 PT_BINDING 331 331 ATP (BY SIMILARITY).
 PT_ACT_SITB 428 428 BY SIMILARITY.
 PT_CONFLICT 199 199 A -> R (IN REF. 1).
 SQ_SEQUENCE 696 AA; 78594 MW; A7B05F5EEAD42AF7 CRC64;

Query Match 24.3%; Score 511.5; DB 1; Length 696;
 Best Local Similarity 36.9%; Pred. No. 1e-27;
 Matches 111; Conservative 63; Mismatches 112; Indels 15; Gaps 7;

QY 11 VFDENEDVNF--DHFEILRAIGKGSFGEVCIVQRNDT**K**AMKYM**N**KQKCVERNEVRNV 68
 DB 288 IYEHEHVRYGPEDFTALRLLIGKGTGQVYLVRKNDTNRIYAMKKISKLIVRKKEVHT 347

QY 69 PKELQIMQGL--EHPFLVNLWYSFODEEDDMFMVVDLGGDLRYHLQONVHFKEETVQL 125
 DB 348 LGERNILVRLTSDESPFIVGLKFSQFATASDLYLITDMSGGELFWLQHEGRPPEQRAKF 407

QY 126 FICELVMLADYLNQRIIHRDMKPDNILLDEHGHVHITDFNIA-AMLPRETOITTMAGTK 184
 DB 408 YIAELVLALEHLHKHDIYRDLKPNENILLDADGHALCDFGLSKANLSANATTNTFCGTT 467

QY 185 PYMAPEMESSRKAGGYSFAVYDWNSLGVTALEYLLGRPYHIRSSTSSKELVHTFETTVVT 244
 DB 468 EYLAPEBVILLEDK--GYTKQVDFWSSLGVLFEMCCGWSFPY---APDVQQMYRNIAFGKVR 522

QY 245 YP-SAWSQEMVSLLKKLLEPNPDQRFSQLSD---VQNFPYMDNDINWDAVFQKRLLPGPIP 300
 DB 523 FPKGVLSSEGGRSFVRGLLNRPNPNHRLGAVADTTTELKEHPPFFADINWDLSSKKVQPPEKPK 582

QY 301 N 301
 DB 583 N 583

RESULT 8
 KAPC_DROME ID P9VTL99; STANDARD; PRT; 352 AA.
 AC P12370; Q9VTL99;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DE CAMP-dependent protein kinase catalytic subunit (EC 2.7.1.37) (PKA C).
 GN PKA-C1 OR CDKA OR DCO OR CG4379.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephdroidea; Drosophilidae; Drosophila.
 NCBI_TAXID=7227;

RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=88115281; PubMed=2828348;
 RX Foster J.L., Higgins G.C., Jackson R.F.;
 RT "Cloning, sequence, and expression of the Drosophila cAMP-dependent
 protein kinase catalytic subunit gene.";
 RL J. Biol. Chem. 263:1676-1681(1988).

RN [2] SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=89107990; PubMed=3215511;
 RT Kalderon D., Rubin G.M.;
 RT "Isolation and characterization of Drosophila cAMP-dependent protein
 kinase genes.";
 RT Genes Dev. 2:1539-1556 (1988).

RN [3] SEQUENCE FROM N.A.
 RP STRAIN=Berkeley;
 RC MEDLINE=20196006; PubMed=10731132;
 RX Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Hendereson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballev R.M., Basu A., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhardari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottner P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,
 RA Fosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy L., Muniz D.M., Nelson D.L.,
 RA Nelson D.R., Neilson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puris V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong P.N., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).

CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- ENZYME REGULATION: Activated by cAMP.
 CC -!- SUBUNIT: Composed of two regulatory chains and two catalytic
 CC -!- chains.
 CC -!- TISSUE SPECIFICITY: More abundant in adult head than adult body.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP
 CC subfamily.

CC -----
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CC -----
 DR EMBL; M18655; AAA28412.1;
 DR EMBL; X16969; CAA34840.1;
 DR EMBL; AB003625; AAF52797.1; -;
 DR PIR; C31751; C31751.
 DR HSSP; P05132; 1ATP.
 DR FlyBase; FBgn000273; Pka-C1.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR GO; GO:0007448; P:anterior/posterior pattern formation, imagi. . . ; IMP.
 DR GO; GO:0019933; P:cAMP-mediated signaling; NAS.
 DR GO; GO:0007456; P:eye morphogenesis (sensu Drosophila); NAS.
 DR GO; GO:0007292; P:female gamete generation; IMP.
 DR GO; GO:0007611; P:learning and/or memory; NAS.
 DR GO; GO:0007480; P:leg morphogenesis (sensu Holometabola); NAS.
 DR GO; GO:0045475; P:locomotor rhythm; NAS.
 DR GO; GO:0008355; P:olfactory learning; NAS.
 DR GO; GO:0007314; P:oocyte anterior/posterior axis determination; IMP.
 DR GO; GO:0008103; P:oocyte microtubule cytoskeleton polarization; IMP.
 DR GO; GO:0008359; P:regulation of bicoid mRNA localization; IMP.
 DR GO; GO:0045473; P:response to ethanol (sensu Insecta); NAS.
 DR GO; GO:0007622; P:rhythmic behavior; IMP.
 DR GO; GO:0007476; P:wing morphogenesis; IMP.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PRO0109; TYRKINASE.
 DR PRODOM; PD000001; Prot kinase; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding; cAMP;
 KW Phosphorylation; Myristate; Lipoprotein.
 FT INIT MET 0 0 BY SIMILARITY.
 FT LIPID 1 1 N-myristoyl Glycine (By similarity).
 FT DOMAIN 45 299 PROTEIN KINASE.
 FT NP BIND 51 59 ATP (BY SIMILARITY).
 FT BINDING 74 74 ATP (BY SIMILARITY).
 FT ACT_SITE 168 168 BY SIMILARITY.
 SQ SEQUENCE 352 AA; 40707 MW; 88E42BCPA95E9640 CRC64;

Query Match 24.3%; Score 510.5; DB 1; Length 352;
 Best Local Similarity 34.4%; Pred. No. 5.5e-28;
 Matches 110; Conservative 72; Mismatches 119; Indels 19; Gaps 6;

Qy 21 DHEFEILRAIGKGSFGEVCIVQKNDTRKMCAMKYMNRKOKCVERNEVRNTPKELQIMQGLEH 80
 Db 43 DDFERIKTLGTGSFGRVMIVQHKPTDYYAMKILDQKVVKLQQVETLINEKRILQAIQF 102
 Qy 81 PFLVNLWYSFQDDEDMFVVDDLLGDLRYHLQQNTVHFKEETVKLPICTELWALDYLQNO 140
 Db 103 PFLVSLRYHFFKDNNSLYMVLLEYVPGGEMFSHLRKVGRFSEPHSRFYAAQIVLAFELYHL 162
 Qy 141 RIIHRDMKPDNILLDEHGHHVHTDPNIAAMLPRETQITTMAGTKPYMAPEMSSRKGAGY 200
 Db 163 DLIVYDLKPEENLLIDSQGLKVTDFGFAKRVKGRRT--WTLGGTPEYLAPEITLSK---GX 217
 Qy 201 SFAVDWWSLGVTAELLRGRRPYHRSSTSKEIIVHTPETV---VTVPSAWSQEMVSLL 257
 Db 2118 NKAVDWWALGVYEMAAGXPFFF-----ADQPIOIYEKIVSGKVPPSHFGSDLKDLL 271
 Qy 258 KKCLEPNPDQRPSQL---SDVQNFPYMNDDINTDAVFOKRLLPGFIPN-KGRLNCDPTFE 312
 Db 272 RNLLQVDLTKRYGNLKAAGVNDLKNQKWFASTDWLAIPOKKIEAPFIPRCKGPDTSNFDD 331

Qy 313 LEEMILESKPLHKKKKRLAK 332
 Db 332 YEEEARISSTEKECAKEFAE 351

RESULT 9
 KAPC_CAEEL_ID KAPC_CAEEL STANDARD; PRT; 404 FA.
 AC P21137; O18310; O18311;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE CAMP-dependent Protein kinase catalytic subunit (BC 2.7.1.37) (PKA C).
 GN KIN-1 OR ZK909.2.
 OS Caenorhabditis elegans.
 OC Rhabditida; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditida; Peloderaiae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN SEQUENCE FROM N.A. (ISOFORM B).
 RC STRAIN=Bristol N2;
 RX MEDLINE=90216721; PubMed=2324104;
 RA Gross R.E., Bagchi S., Lu X., Rubin C.S.;
 RT "Cloning, characterization, and expression of the gene for the
 catalytic subunit of cAMP-dependent protein kinase in *Caenorhabditis*
 elegans. Identification of highly conserved and unique isoforms
 generated by alternative splicing.",
 RT

RL J. Biol. Chem. 265:6896-6907 (1990).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA White S., McLay K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
 [3]
 RN REVISIONS, AND ALTERNATIVE SPlicing.
 RA Durbin R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Composed of two regulatory chains and two catalytic chains.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=13;
 CC Comment=Experimental confirmation may be lacking for some
 CC isoforms;
 CC Name=a; Sequence=Major;
 CC Name=b; Sequence=VSP_004751, VSP_004758;
 CC Name=c; Sequence=VSP_004752, VSP_004756, VSP_004757;
 CC Name=d; Sequence=VSP_004751;
 CC Name=e; Sequence=VSP_004750;
 CC Name=f; Sequence=VSP_004752, VSP_004758;
 CC Name=g; Sequence=VSP_004754, VSP_004758;
 CC Name=h; Sequence=VSP_004753;
 CC Name=i; Sequence=VSP_004753;
 CC Name=j; Sequence=VSP_004754;
 CC Name=k; Sequence=VSP_004753;
 CC Name=l; Sequence=VSP_004755;
 CC Name=m; Sequence=VSP_004758;
 CC Name=n; Sequence=VSP_004758;
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP
 CC
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CC DR EMBL; M37119; AAA51610.1; -.
 CC DR EMBL; M37114; AAA51610.1; JOINED.
 CC DR EMBL; M37115; AAA51610.1; JOINED.
 CC DR EMBL; M37116; AAA51610.1; JOINED.
 CC DR EMBL; M37117; AAA51610.1; JOINED.
 CC DR EMBL; M37118; AAA51610.1; JOINED.
 CC DR EMBL; Z82096; CAD45613.1; -.
 CC DR EMBL; Z82096; CAD45614.1; -.
 CC DR EMBL; Z82096; CAD45615.1; -.
 CC DR EMBL; Z82096; CAD45616.1; JOINED.
 CC DR EMBL; 281511; CAD45616.1; JOINED.
 CC DR EMBL; 282096; CAD45617.1; -.
 CC DR EMBL; 281511; CAD45617.1; JOINED.
 CC DR EMBL; 282096; CAD45618.1; JOINED.
 CC DR EMBL; 281511; CAD45619.1; -.
 CC DR EMBL; 281511; CAD45619.1; JOINED.
 CC DR EMBL; 282096; CAD45620.1; JOINED.
 CC DR EMBL; 281511; CAD45620.1; JOINED.

DR	EMBL; Z82096; CAD45621.1;	FT	FT
DR	EMBL; Z81511; CAD45621.1;	FT	FT
DR	EMBL; Z82096; CAD45622.1;	FT	FT
DR	EMBL; Z81511; CAD45622.1;	FT	FT
DR	EMBL; Z82096; CAD45623.1;	FT	FT
DR	EMBL; Z81511; CAD45623.1;	FT	FT
DR	EMBL; Z82096; CAB05034.1;	FT	FT
DR	EMBL; Z81511; CAB05034.1;	FT	FT
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DR	EMBL; Z82096; CAD45587.1;	FT	FT
DR	EMBL; Z81511; CAD45587.1;	FT	FT
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DR	EMBL; Z82096; CAD45589.1;	FT	FT
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DR	EMBL; Z82096; CAD45590.1;	FT	FT
DR	EMBL; Z81511; CAD45590.1;	FT	FT
DR	PIR; A35755; OKRWCl.	FT	FT
DR	PIR; B35755; OKRWCl2.	FT	FT
DR	PIR; T21211; T21211.	FT	FT
DR	PIR; T21212; T21212.	FT	FT
DR	HSSP; P05132; 1ATP.	FT	FT
DR	WormPep; ZK909.2a; CE15473.	FT	FT
DR	WormPep; ZK909.2b; CE15475.	FT	FT
DR	WormPep; ZK909.2c; CE31755.	FT	FT
DR	WormPep; ZK909.2d; CB31756.	FT	FT
DR	WormPep; ZK909.2e; CE31757.	FT	FT
DR	WormPep; ZK909.2f; CE31758.	FT	FT
DR	WormPep; ZK909.2g; CE31759.	FT	FT
DR	WormPep; ZK909.2h; CE31760.	FT	FT
DR	WormPep; ZK909.2i; CE31761.	FT	FT
DR	WormPep; ZK909.2j; CE31762.	FT	FT
DR	WormPep; ZK909.2k; CE31763.	FT	FT
DR	WormPep; ZK909.2l; CE31764.	FT	FT
DR	InterPro; IPR000719; Prot_kinase.	FT	FT
DR	InterPro; IPR002290; Ser_thr_pk kinase.	FT	FT
DR	InterPro; IPR001245; Tyr_pk kinase.	FT	FT
DR	Pfam; PF00069; pkinase; 1.	FT	FT
DR	PRINTS; PR00109; TYRKINASE.	FT	FT
DR	PRODOM; PD000001; Prot_kinase; 1.	FT	FT
DR	SMART; SM00220; S_TKc; 1.	FT	FT
DR	SMART; SM00219; Tyrkc; 1.	FT	FT
DR	PROSITE; PS50011; PROTEIN_KINASE_ATP; 1.	FT	FT
DR	PROSITE; PS500108; PROTEIN_KINASE_ST; 1.	FT	FT
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; cAMP;	FT	FT
KW	Phosphorylation; Alternative splicing.	FT	FT
DOMAIN	81 335 PROTEIN KINASE.	FT	FT
FT	NP_BIND 87 95 ATP (BY SIMILARITY).	RESULT 10	
FT	BINDING 110 110 ATP (BY SIMILARITY).	KAPA_CRIGR	
FT	ACT_SITE 204 204 BY SIMILARITY.	ID_KAPA_CRIGR	
FT	MOD_RES 233 233 PHOSPHORYLATION (POTENTIAL).	AC_P25321;	
FT	MOD_RES 376 376 MPTRLDIVGNLQFSSSTDNGDEDQADVTACFVLPSPPSSFS	DT_01-MAY-1992 (Rel. 22, Created)	
FT	VARSPLIC 1 52 KLSIILDDDPVFD -> MSSSSNNKKVQVKP (in isoform m).	DT_01-MAY-1992 (Rel. 22, Last sequence update)	
FT		DT_10-OCT-2003 (Rel. 42, Last annotation update)	
FT		DE_CAMP-dependent protein kinase, alpha-catalytic subunit (EC 2.7.1.37)	
FT		DB (PKA C-alpha).	
VARSPLIC	1 53 MPTRLDIVGNLQFSSSTDNGDEDQADVTACFVLPSPPSSFS	PRT; 350 AA.	

kinase complexed with MgATP and peptide inhibitor.";

RL Biochemistry 32:2154-2161(1993).

-!- FUNCTION: Phosphorylates a large number of substrates in the cytoplasm and the nucleus.

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-!- ENZYME REGULATION: Activated by cAMP.

-!- SUBUNIT: A number of inactive tetrameric holoenzymes are produced by the combination of homo- or heterodimers of the different regulatory subunits associated with two catalytic subunits. cAMP causes the dissociation of the inactive holoenzyme into a dimer of regulatory subunits bound to four cAMP and two free monomeric catalytic subunits.

-!- SUBCELLULAR LOCATION: Cytoplasmic (inactive holoenzyme and monomeric catalytic subunit). Translocates into the nucleus (monomeric catalytic subunit) (By similarity).

-!- TISSUE SPECIFICITY: Ubiquitously expressed in mammalian tissues.

-!- PTM: Asn-2 is deaminated in Asp-2 in more than 25% of the proteins, giving rise to 2 major isolectric variants, called CB and CA respectively (0.4 pH unit change). Deamidation proceeds via the so-called beta-aspartyl shift mechanism and yields either D-Asp-2 (major) or D-isoAsp-2 (minor), in addition to L-isomers. Deamidation occurs after the addition of myristate. The Asn-2 form reaches a significantly larger nuclear/cytoplasmic ratio than the Asp-2 form.

-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.

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QY	79	EHPPFLVNLWYSFQDEEDDMFMVV DLLGDLRHYLQQMVTHFKEETVKLFICBLVMA LDYLQ	138
Db	99	NFPFLVKLEYSFKDNSNLYMMEYVPGGEMFSHLRRIGREFSEPHARFYAAQIVLTFBXLH	158
QY	139	NQRIIHRDMKPDNILLDEHGHVHITDFNIAAMILPRETQITTMAGTKP YMAPBEMFSSRKG A	198
Db	159	SLDLIYRDLKPBNNLLIDQQGYIQVTDFGFAKRVKGRT -WTL CGTP EYLAP EIIILSK--	213
QY	199	GYSFAVDWWSSLGV TAYELLRGR RPYH I R SSSKEIV H T FETTV --V T Y P S A W S Q E M V S	255
Db	214	GYNKAVDWWALGVLIYEMAAGYPPPF----ADQPIQIYEKIVSGKVR F P S H E F S S D L K D	267
QY	256	L L K K L L E P N P D O R P S Q L ----S DV Q N F P M M D I N W D A V F Q K R L I P G P I P N - K G	303
Db	268	LLRNLLQV DLT KRG N L I Q N G V N D I K N H K W F A T T D W I A I Y Q R K V E A P P I P K F K G	320
RESULT 12			
SCH9 YEAST			
ID	SCH9 YEAST	STANDARD;	PRT;
AC	P11792;		823 AA.
DT	01-OCT-1989 (Rel. 12, Created)		
DT	01-FEB-1995 (Rel. 31, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DB	Serine/threonine-protein kinase SCH9 (EC 2.7.1.37).		
GN	SCH9 OR KOM1 OR YHR205W.		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces.		
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.		
NCBI_TaxID	=4932;		
RN			
RP	SEQUENCE FROM N.A. MEDLINE=88255839; PubMed=3290050;		
RX	Toda T., Cameron S., Sass P., Wigler M.;		
RA	"SCH9, a gene of <i>Saccharomyces cerevisiae</i> that encodes a protein distinct from, but functionally and structurally related to, cAMP-		
RT	dependent protein kinase subunits."		
RT	<i>Genes Dev.</i> 2:517-527(1988).		
RL	[2]		
RN	SEQUENCE FROM N.A. RP STRAIN=JR26-19D;		
RC	MEDLINE=93182531; PubMed=8442384;		
RX	di Blasi F., Carra E., Venditti B., Masturzo P., Burderi E.,		
RA	Lambrinoudaki I., Mirisola M.G., Seidita G., Fasano O.;		
RA	"The SCH9 protein kinase mRNA contains a long 5' leader with a small open reading frame."		
RT	<i>Yeast</i> 9:21-32(1993).		
RL	[3]		
RN	SEQUENCE FROM N.A. RP STRAIN=S288C / AB972;		
RC	MEDLINE=94378003; PubMed=8091229;		
RX	Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,		
RA	Du Z., Favelllo A., Fulton L., Gattung S., Geisel C., Kirsten J.,		
RA	Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,		
RA	Latreille P., Louis E.J., Macri C., Mardis E., Menevez S., Mouser L.,		
RA	Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis B., Vaughan K.,		
RA	Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,		
RA	Vaudin M.;		
RT	"Complete nucleotide sequence of <i>Saccharomyces cerevisiae</i> chromosome VIII."		
RT	<i>Science</i> 265:2077-2082(1994).		
CC	-/- FUNCTION: Protein kinase that is part of growth control pathway which is at least partially redundant with the cAMP pathway.		
CC	-/- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.		
CC	-/- ENZYME REGULATION: Activated by cAMP.		
CC	-/- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. CAMP subfamily.		
CC	-/- SIMILARITY: Contains 1 C2 domain.		

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RESULT 13
 K6A3_HUMAN STANDARD; PRT; 740 AA.
 ID K6A3_HUMAN STANDARD; PRT; 740 AA.
 AC P51812;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Ribosomal protein S6 kinase alpha 3 (EC 2.7.1.37) (S6K-alpha 3) (90 kDa ribosomal protein S6 kinase 3) (p90-RSK 3) (Ribosomal S6 kinase 2) (RSK-2) (pp90RSK2) (Insulin-stimulated protein kinase 1) (ISPK-1).
 DB RPS6KA3 OR RSK2 OR ISPK1.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta, and T-cell;
 RX MEDLINE=95113220; PubMed=7813820;
 RA Bjoerbaek C., Vik T.A., Eichwald S.M., Webb G.C., Wang J.P., Yang P.-Y., Vestergaard H., Richmon K., Hansen T., Erikson R.L., Miklos G.L.G., Cohen P.T.W., Pedersen O.;
 RT "Cloning of a human insulin-stimulated protein kinase (ISPK-1) gene and analysis of coding regions and mRNA levels of the ISPK-1 and the protein phosphatase-1 genes in muscle from NIDDM patients.";
 RT diabetes 44:90-97(1995).
 RL [2]
 RN SEQUENCE OF 2-582 FROM N.A.
 RP TISSUE=Skeletal muscle;
 RX MEDLINE=94189676; PubMed=8141249;
 RA Moller D.E., Xia C.-H., Tang W., Zhu A.X., Jakubowski M.;
 RT "Human Rsk isoforms: cloning and characterization of tissue-specific expression.";
 RT Am. J. Physiol. 266:C351-C359(1994).
 RL [3]
 RN VARIANTS CLS VAL-75 AND ALA-227.
 RP MEDLINE=97113410; PubMed=8955270;
 RX Trivier E., de Cesare D., Jacquot S., Pannetier S., Zackai E., Young I., Mandel J.-L., Sascone-Corsi P., Hanauer A.;
 RA RT "Mutations in the kinase Rsk-2 associated with Coffin-Lowry syndrome.";
 RT RL Nature 384:567-570(1996).
 RN [4]
 RP VARIANTS CLS PHE-82; GLN-127; TYR-154; VAL-225 AND ASP-431, AND VARIANT SER-38.
 RP MEDLINE=9905750; PubMed=9837815;
 RX Jacquot S., Merienne K., de Cesare D., Pannetier S., Mandel J.-L., RA RT "Novel mutations in Rsk-2, the gene for Coffin-Lowry syndrome (CLS)." ;
 RT extensive allelic heterogeneity and a high rate of de novo mutations.";
 RT RL Am. J. Hum. Genet. 63:1631-1640(1998).
 RN [5]
 RP VARIANTS CLS TRP-114 AND GLN-729.
 RX MEDLINE=99191975; PubMed=10094187;
 RA Abidi F., Jacquot S., Lassitter C., Trivier E., Hanauer A., Schwartz C.E.;
 RT "Novel mutations in Rsk-2, the gene for Coffin-Lowry syndrome (CLS)." ;
 RT RL Eur. J. Hum. Genet. 7:20-26(1999).
 CC -!- FUNCTION: Phosphorylates a wide range of substrates including
 CC -!- ribosomal protein S6. Implicated in the activation of the mitogen-
 CC -!- activated kinase cascade.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- TISSUE SPECIFICITY: Expressed in many tissues, highest levels in
 CC skeletal muscle.
 CC -!- DISEASE: Defects in RPS6KA3 are the cause of Coffin-Lowry syndrome (CLS) [MIM:303600]; an X-linked dominant disorder characterized by severe mental retardation with facial and digital dysmorphisms, and progressive skeletal deformations.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6
 CC kinase subfamily.
 CC
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CC	EMBL; U08316; AAA81952.1; -.	Db	56 VKEGHKADPSQFELLKVKGQGSFGKVFLVKKISGSNDARQLYANKVULKKKATLKVRDRVRT 115
CC	EMBL; L07599; AAC82495.1; -.	Qy	68 VFKELOQIMQGLEHPFLVNLMYSFODEEDMFMVDLLGGDLRYHQQNQVHFKEETVKLFPI 127
CC	DR PIR; I38556; I38556.	Db	116 KM-ERDILVEVNHPRIVKLYAFQTEGKLVLIDFLRGGLFTRLSKEVMFTTEBDVKFYL 174
CC	DR HSSP; Q63450; 1A06.	Qy	128 CELVMALDYLONORI IHRDMKPDNILLDEGHVHITDFNIA-AMLPRETOQTTMAGTKPY 186
CC	DR Genew; HGNC:10432; RPS6KA3.	Db	175 ABLLAALDHLHSLGIIYRDLKPENILDEGEHKLTDFLGSKESIDHEKKAYSPCGTVEY 234
CC	DR MIM; 300075; -.	Qy	187 MAPEMFSSRKKGAGYSEFAVDWNSLGVTAYELLOWRGRRPYHRSSTSSEIVHTFETTVVTYP 246
CC	DR MIM; 303600; -.	Db	235 MAPEVNR---GHTQSADWWSPGVLMFEMLTGTLPF---QGKDORKETMTMILKAKLGMP 288
CC	DR GO; GO:0004674; P:protein serine/threonine kinase activity; TAS.	Qy	247 SAWQEMNTSLLKKLEPNPNDQRFSQ----LSDVYQNFPMYMDINWDAVFQKRLLPGFIPNK 302
CC	DR GO; GO:0007417; P:central nervous system development; TAS.	Db	289 QFLSPEAQSSLRLMLFKRNPAANRLGAGPDGVBEEIKRHSEFFSTIDWNKLYRREIHPPFKPAT 348
CC	DR GO; GO:0007165; P:signal transduction; TAS.	Qy	303 GR----LNCDPTP 311
CC	DR GO; GO:0001501; P:skeletal development; TAS.	Db	349 GRPEDTYYFDPEF 361
CC	DR InterPro; IPR000961; Pkinase_C.	RESULT 14	K6A3_MOUSE
CC	DR InterPro; IPR000719; Prot kinase.	ID	K6A3 MOUSE STANDARD;
CC	DR InterPro; IPR008271; Ser_Thr_pkin_AS.	AC	P03140; Q8K3J8;
CC	DR InterPro; IPR002290; Ser_thr_pkinase.	DT	01-NOV-1990 (Rel. 16, Created)
CC	DR InterPro; IPR001245; Tyr_pkinase.	DT	10-OCT-2003 (Rel. 42, Last sequence update)
CC	DR InterPro; IPR00069; pkinase_2.	DT	15-MAR-2004 (Rel. 43, Last annotation update)
CC	DR Pfam; PF00433; pkinase_C; 1.	DE	Ribosomal protein S6 kinase alpha 3 (EC 2.7.1.37) (S6K-alpha 3) (90 kDa ribosomal protein S6 kinase 3) (p90-RSK 3) (Ribosomal S6 kinase 2)
CC	DR PRINTS; PR00109; TYRKINASE.	DE	(RSK-2) (pp90RSK2) (MAP kinase-activated protein kinase 1b) (MAPKAPK1B).
CC	DR ProDom; PD000001; Prot_kinase; 2.	DB	RPS6KA3 OR RSK2 OR RPS6KA-RS1.
CC	DR SMART; SMART00133; S_TK_X_1.	GN	Mus musculus (Mouse).
CC	DR SMART; SMART00220; S_TKC; 2.	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 2.	OC	OC
CC	DR PROSITE; PS00108; PROTEIN_KINASE_ST; 2.	OC	OC
CC	DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.	NCBI_TAXID	NCBI_TAXID=10090;
CC	KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat; Multigene family; Disease mutation; Polymorphism.	RN	[1]
CC	FT DOMAIN 68 327 PROTEIN KINASE 1.	RP	SEQUENCE FROM N.A.
CC	FT DOMAIN 422 679 PROTEIN KINASE 2.	RX	PubMed=12016217;
CC	FT NP_BIND 74 82 ATP (BY SIMILARITY).	RA	Chrestensen C.A., Sturgill T.W.,
CC	FT BINDING 100 100 ATP (BY SIMILARITY).	RT	"Characterization of the p90 ribosomal S6 kinase 2 carboxyl-terminal domain as a protein kinase.";
CC	FT ACT SITE 193 193 BY SIMILARITY.	RL	J. Biol. Chem. 277:27733-27741 (2002).
CC	FT NP_BIND 428 436 ATP (BY SIMILARITY).	RN	[2]
CC	FT BINDING 451 451 ATP (BY SIMILARITY).	RP	SEQUENCE OF 108-740 FROM N.A.
CC	FT ACT SITE 539 539 ATP (BY SIMILARITY).	RX	PubMed=89384612; PubMed=2779569;
CC	FT VARIANT 38 38 BY SIMILARITY.	RA	Alcorta D.A., Crews C.M., Sweet L.J., Bankston L., Jones S.W., Erikson R.L.;
CC	I -> S.	RT	"Sequence and expression of chicken and mouse rsk: homologs of Xenopus laevis ribosomal S6 kinase."
CC	/FTId=VAR_006188.	RL	Mol. Cell. Biol. 9:3850-3859(1989).
CC	G -> V (IN CLS).	CC	-1- FUNCTION: Serine/threonine kinase that may play a role in mediating the growth-factor and stress induced activation of the transcription factor CREB (By similarity).
CC	/FTId=VAR_006189.	CC	-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC	V -> F (IN CLS).	CC	-1- COFACTOR: Magnesium (By similarity).
CC	/FTId=VAR_006190.	CC	-1- ENZYME REGULATION: Activated by multiple phosphorylations on threonine and serine residues (By similarity).
CC	R -> W (IN CLS).	CC	-1- SUBUNIT: Forms a complex with either ERK1 or ERK2 in quiescent cells. Transiently dissociates following mitogenic stimulation (By similarity).
CC	/FTId=VAR_006191.	CC	-1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6 kinase subfamily.
CC	H -> Q (IN CLS).	CC	-1- TISSUE SPECIFICITY: Intestine, thymus, lung, heart and brain.
CC	/FTId=VAR_006192.	CC	-1- PTM: Autophosphorylated on Ser-386, as part of the activation process (By similarity).
CC	D -> Y (IN CLS).	CC	-1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. S6 kinase subfamily.
CC	/FTId=VAR_006193.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
CC	A -> V (IN CLS).	CC	the European Bioinformatics Institute.
CC	/FTId=VAR_006194.	CC	
CC	S -> A (IN CLS).	CC	
CC	/FTId=VAR_006195.	CC	
CC	G -> D (IN CLS).	CC	
CC	/FTId=VAR_006196.	CC	
CC	R -> Q (IN CLS).	CC	
CC	/FTId=VAR_006197.	CC	
CC	V -> L (IN REF. 2).	CC	
CC	CONFICT 424 424 K -> N (IN REF. 2).	CC	
CC	CONFICT 480 480 MISSING (IN REF. 2).	CC	
CC	CONFICT 494 494 MW: 486AE8357CEAB6C8 CRC64;	CC	
CC	SEQUENCE 740 AA; 83736 MW: 486AE8357CEAB6C8 CRC64;	CC	
CC	Query Match 23.8%; Score 501.5; DB 1; Length 740;	CC	
CC	Best Local Similarity 35.1%; Pred. No. 5.4e-27;	CC	
CC	Matches 110; Conservative 66; Mismatches 118; Indels 19; Gaps 7;	CC	
CC	11 VFDENEDVNFDHFLRAIGKGSFGEVCIVQK--NDTKQMCAMKYMNKQKCVERNEVRN 67	CC	

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RESULT 15
 YPK2 - YEAST ID: YPK2_YEAST STANDARD; PRT; 677 AA.
 AC P18961;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Serine/threonine-protein kinase YPK2/YKR2 (EC 2.7.1.-).
 GN YPK2 OR YKR2 OR YMR104C OR YM9718.03C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces;
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 MBMLINB=89306654; PubMed=2663649;
 RX Kubo K., Ohno S., Matsumoto S., Yahara I., Suzuki K.;
 RA "A novel yeast gene coding for a putative protein kinase.";
 RT RL Gene 76:177-180(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 MBMLINB=93173125; PubMed=8437590;
 RX Chen P.C., Lee K.S., Levin D.E.;
 RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
 RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
 RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
 RT RL Mol. Gen. Genet. 236:443-447(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 STRAIN=S288C / AB972;
 RC MBMLINB=97313268; PubMed=9169872;
 RX Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
 RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
 RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
 RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
 RT RL Mol. Gen. Genet. 236:443-447(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 DR PROSITE: PS00107; PROTBIN_KINASE_ATP; 2.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 2.
 DR PROSITE: PS50011; PROTBIN_KINASE_DOM; 2.
 DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;
 KW Repeat; Multigene family; Phosphorylation;
 FT DOMAIN 68 327 PROTEIN KINASE 1.
 FT DOMAIN 422 679 PROTEIN KINASE 2.
 FT NP BINDING 74 82 ATP (BY SIMILARITY).
 FT PT BINDING 100 100 ATP (BY SIMILARITY).
 FT ACT SITE 193 193 BY SIMILARITY.
 FT NP BIND 428 436 ATP (BY SIMILARITY).
 FT PT BINDING 451 451 ATP (BY SIMILARITY).
 FT ACT SITE 539 539 "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XIII."
 FT MOD RES 227 227 Nature 387:90-93 (1997).
 FT MOD RES 365 365 -1- FUNCTION: Plays an essential role in the proliferation of yeast
 FT MOD RES 369 369 cells.
 FT MOD RES 386 386 -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 FT MOD RES 577 577 RAC SUBFAMILY. STRONGEST TO YPK1.
 FT MOD RES 737 737 GermOnline: 142772; -.
 SQ SEQUENCE 740 AA; 83693 MW; 0CD54B5918567007 CRC64;
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 CC
 CC Query Match 23.8%; Score 501.5; DB 1; Length 740;
 CC Best Local Similarity 35.1%; Pred. No. 5.4e-27;
 CC Matches 110; Conservative 66; Mismatches 118; Indels 19; Gaps 7;
 CC
 Qy 11 VFDENEDVNFDPEIILRAIGKGSFGEVCIVKQ---NDTKKKMCKAMKYMNQKCVERNEVRN 67
 Db 56 VKEGHEKADPSQFELLKVLGQSFKGKFVFLVKKISGSDARQLYAMKVLKATLKVRDRVRT 115
 Qy 68 VPKBLQIMQGLEHPPFLVNLWYSQDDEDMFMVVDDLLGGDLRYHLQQNVTHPKBTETKLPI 127
 Db 116 KM-ERDILVEVNHPPFTVKLYHAQFTEGKLYLILDFLRGGDFTRLSKEVMFTEDVKFYL 174
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR EMBL; 249702; CAA89740.1; -.
 DR PIR; JS0178; JS0178.
 DR HSSP; P05132; ICTP.
 DR SGD; S0004710; YPK2.
 DR SMART; SM00133; S_TK_X; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR SMART; SM00220; S_TK_C; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferase; Serine/threonine-protein kinase; ATP-binding.
 PT DOMAIN 35 57 HIS-RICH.
 PT DOMAIN 344 599 PROTEIN KINASE.

```

PT NP BIND      350      358      ATP (BY SIMILARITY).
PT BINDING    373      373      ATP (BY SIMILARITY).
PT ACT SITE   467      467      BY SIMILARITY.
SQ SEQUENCE   677 AA; 76664 MW; EIFAB0295386A113 CRC64;

Query Match      23.8%; Score 501; DB 1; Length 677;
Best Local Similarity 32.5%; Pred. No. 5.2e-27;
Matches 116; Conservative 76; Mismatches 127; Indels 38; Gaps 10;

Qy   8 KPPVFDENEDVNFDFBILRAIGKGSFGEVCTIVQVNNDTRKCAMKRYMNKOKCVERNEVRN 67
Db 332 KP---SKRKPLSIDDFFDLRKVIGKGSFHKVGMQRKKDTQKIYALKALRKAYIVSKCEVTH 388

Qy   68 VFKELQIMOGLEHPFLVNLWYSFQDEEDDMFMVVDLGGDLRYHLQQNVHFKETVVLFTI 127
Db 389 TLAERTVLLARVDCPFPVPLKPSPOSPEKLYLVAFTINGGELFYHLQHEGRFLSLARSRFYI 448

Qy   128 CBLVMAVDYLQNQRIIHMDMKPDNILLDEHGHVHHTIDFNIAAMLPRETQT-TMAGTKPY 186
Db 449 AELLCALDSLHKLDVYRDLKPENILLDYQGHIALCDFGLCKLMKDNDKTDTFCGTPY 508

Qy   187 MAPEMFSSRKGAGYSFAVDWISLGVTAYELLRGRRPYHIRS-STSSKEIVHTFETTVVTY 245
Db 509 LAPEIL--LGQGYTKTVDWWTLGILLYEMMTGLLPPYYDENVPVMYKKLQ---QPLLF 561

Qy   246 PSAWSQEMVSLLKKLLEPNPDQRF--SQLSDVQNFPMNDINWDAVFQKRLLPGFIPNKG 303
Db 562 PDGFDPAAKDLLIGLSSRDBSRRRLGVNGTDEIRNHPFFKDISH---KQLLLRGYIP--- 614

Qy   304 RLNCDPTELEEMILESKPLHKKKKRLLAKKEKDMRKCDSSQTCLLQEHLDSVQKEF 359
Db 615 -----PYKPIVKSEIDTANFDDQEFRK-EKPIDSVVDEYLSASIQKQF 655

```

Search completed: June 25, 2004, 10:49:36
 Job time : 20 secs

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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:46:29 ; Search time 21 Seconds

(without alignments)
 1813.897 Million cell updates/sec

Title: US-10-667-442-2

Perfect score: 2104

Sequence: 1 MGANTSRKPPVFDENEDVNFI.....NLALEQTQDQGEDQNNNL 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 Seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78:*

pir1:*

pir2:*

pir3:*

pir4:*

RESULT 1

T23688

hypothetical protein M03C11.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #text_change 31-Jan-2000

C;Accession: T23688

R;McMurray, A.

submitted to the EMBL Data Library, April 1995

A;Reference number: 219783

A;Accession: T23688

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-379 <WIL>

A;Cross-references: EMBL:Z49128; PIDN:CAA88953.1; GSPDB:GN00021; CESP:M03C11.1

A;Experimental source: clone M03C11

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Genetics:

protein kinase 2 (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)
 C;Species: Dictyostelium discoideum
 C;Accession: A38578
 R;Haribabu, B.; Dottin, R.P.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991
 A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum
 A;Reference number: A38578; MUID:91142122; PMID:1996312
 A;Accession: A38578
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-479 <HAR>
 A;Cross-references: GB:M59744; PIDN:AAA33186.1; PID:g167718
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine
 P;151-407/Domain: protein kinase homology <KIN>
 P;159-167/Region: protein kinase ATP-binding motif

Query Match 25.1%; Score 528.5%; DB 1; Length 648;
 Best Local Similarity 34.2%; Pred. No. 7.5e-17;
 Matches 110; Conservative 76; Mismatches 115; Indels 21; Gaps 8;

Qy 9 PPVFDENEDVNFDHFELRAIGKGSFGEYCVIQKNDTCKMC--AMKXMKQKCVERNEVR 66
 Db 325 PPV---NARERLKEPKQIRVLGTGKTYLIQ--NTKDGCYAMKCLNKAYVQLQVE 379

Qy 67 NVPKELQIMQGLEHPFLVNLWYSFQDEBDMFMVVDLILGGDLRYHLQQNTVHFKETTVKL 126
 Db 380 HINSEKSILSSIIHPPFIVNLXQAQFQDKEKCLYLFFBYVAGGBEVTHLRKSMKFNSNSTAKFY 439

Qy 127 ICELVMALDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQTITTMAGTKPY 186
 Db 440 AAEIVVLALEFLHKRQNTIVRDLKPENLILDNQGHIKITDFGFAKRV--BDRFTFLCGTPFY 497

Qy 187 MAPEMFSSRKGAGYSFAVDWWSLGVTALEYLLRGRPYHRSSTSKEIVHTFTVVVTYP 246
 Db 498 LAPBIIQSK--GHGKCAVDWWAIGLILPFEMLAGYPFPY---DDDTTPAIYNKILLAGRIFP 551

Qy 247 SAWSQEMVSLLKKLLEPNPDQRFSQSL---DVQNPFPYMDINWDAVFQKRKLIPGPINK 302
 Db 552 LGFDVDAKDLIKRLLTADRTRLGALKDGDVKHWFSDINWERYLQRRDNGPFPIRKI 611

Qy 303 RLNCDPPTFBL--EMILES KPL 322
 Db 612 QHQGDSNSNPEMYDBEEMVEEPP 633

RESULT 4
 S56639 ribosomal protein S6 kinase homolog (clone Aspkl1) - oat
 N;Alternate names: mitogen-activated protein kinase pp70 homolog
 C;Species: Avena sativa (oat)
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
 C;Accession: S56639
 R;Buttly, A.K.; Phillips, A.L.
 Plant Mol. Biol. 27, 1043-1052, 1995
 A;Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that s
 A;Reference number: S56638; MUID:95284341; PMID:7766874
 A;Accession: S56639
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-480 <HUT>
 A;Cross-references: EMBL:X79992; PID:9871985; PIDN:CAA56313.1; PID:g871986
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C;Keywords: Arp; phosphotransferase; protein kinase
 P;149-407/Domain: protein kinase homology <KIN>
 P;157-165/Region: protein kinase ATP-binding motif

Query Match 24.8%; Score 521; DB 2; Length 480;
 Best Local Similarity 35.3%; Pred. No. 1.2e-16;
 Matches 107; Conservative 62; Mismatches 124; Indels 10; Gaps 3;

Qy 14 ENEDVNFDPDHFELRAIGKGSFGEYCVIQKNDTCKMCAMKYMNKQKCVERNEVR 73
 Db 142 ENEAVGLDNFPEVLLKGQGAFFGKVYQVRMKGTSEIYAMKVMRKDKILEKQHAEYMAKA RD 201

Qy 74 IMQGLEHPFLVNLWYSFQDEBDMFMVVDLILGGDLRYHLQQNLFRSETVKLPLICLVM 133
 Db 202 ILTKVDHPFVQLRYSFQTKYRLVLFQVNGGHLFFPQLYQOGLFREBLARIYTAEIVSA 261

RESULT 3
 JQ1150 protein kinase (EC 2.7.1.37) cAMP-dependent, catalytic chain - slime mold (Dictyostelium discoideum)
 C;Species: Dictyostelium discoideum
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 24-Apr-1998
 C;Accession: JQ1150
 R;Buerki, E.; Anjard, C.; Scholder, J.C.; Raymond, C.D.
 Gene 102, 57-65, 1991
 A;Title: Isolation of two genes encoding putative protein kinases regulated during Dictyostelium discoideum
 A;Reference number: JQ1150; MUID:91323730; PMID:1864510
 A;Accession: JQ1150
 A;Molecule type: DNA
 A;Residues: 1-648 <BU>
 A;Cross-references: GB:M38703
 C;Genetics:
 A;Gene: PK2
 A;Introns: 578/3
 C;Complex: heterodimer with regulatory chain; active catalytic chain is released when cA
 C;Function:
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 A;Note: important for cell type differentiation and fruiting body morphogenesis
 C;Superfamily: Dictyostelium cAMP-dependent protein kinase catalytic chain; protein kinase
 C;Keywords: Arp; magnesium; phosphoprotein; phosphotransferase; serine/threonine-specific
 P;126-223/Region: glutamine-rich
 F;297-312/Region: glutamine-rich
 F;334-590/Region: protein kinase homology <KIN>

Qy 134 LDYLQNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQTITTMAGTKPYMAPEMS 193
 Db 262 VAHLHANGIMERDLKPENILLDARGHAMLTDFGLAKEFDENTRNSMCGTVEYMAPIV- 320

Qy 194 SRKGAGGSFAVDWWSLGVTALEYLLRGRPYHRSSTSKEIVHTFTVVVTYPSAWSQEM 253
 Db 321 --QGRGHDKADWWSVGILLFEMLTGKPPF---GGRDQKIQQQKIVREKMQKPSYLESER 375

Qy 254 VSLLKLLPEPNPDRQFSQ---LSDVQNPYMNNDINWDAVFQKRLIIPGFIIPNKGRLNCDP 309
 Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 376 HSLKGGLHKEACKRKLGSGLGGSDIEKHNWKWFKAIVNWKLEARQIQPSFCPCNVAGQTCA 435

Qy 310 TFE 312
 Db 436 NFD 438

RESULT 5

S68462 protein kinase ATPK6/ATPK1 (EC 2.7.1.-) - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
 C;Accession: S68462; A54141
 R;Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
 PEBS Lett. 358, 199-204, 1995
 A;Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold
 A;Reference number: S68462; MUID:95129712; PMID:7828736
 A;Accession: S68462
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-465 <MIZ>
 A;Cross-references: EMBL:D42056; NID:9867996; PIDN:BAA07656.1; PID:d1008238; PID:9867997
 R;Zhang, S.H.; Lawton, M.A.; Hunter, T.; Lamb, C.J.
 J. Biol. Chem. 269, 17586-17592, 1994
 A;Title: atpk1, a novel ribosomal protein kinase gene from *Arabidopsis*. I. Isolation, ch
 A;Reference number: A54141; MUID:94292519; PMID:7912697
 A;Contents: ecotype Landsberg erecta
 A;Accession: A54141
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-465 <ZHA>
 A;Cross-references: GB:L29030; NID:9508307; PIDN:AAA21142.1; PID:9508308
 A;Note: sequence extracted from NCBI backbone (NCBIN:149344, NCBIPI:149415)
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 P;132-389/Domain: protein kinase homology <KIN>
 P;140-148/Region: protein kinase ATP-binding motif
 A;Molecule type: DNA
 A;Residues: 1-465 <ZHA>

Query Match 24.5%; Score 516.5; DB 2; Length 465;
 Best Local Similarity 34.1%; Pred. No. 1.9e-16;
 Matches 102; Conservative 66; Mismatches 120; Indels 11; Gaps 3;

Qy 18 VNFDHFIELRAIGKGSFGEYCVIQKNNDTKKMCAMKYMNNKKQKCVERNEVRNFKELQIMQG 77
 Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 129 VGIDDFEVMKVVGKGAFFGVYQVRKKEITSEIYAMKVMRKDHIMEXNHAEYMAERDILTK 188
 Qy 78 LEHPLFLVNLYSFQDEEDMFMYVDDLLGGDLRYHLQQNQVHFKEETVYLKFCICELYMAIDYL 137
 Db 189 IDHPEFIVQLKYSFQTKYRLVLVLDINGGHFLFQYQHQLFREDLARVYTAVSAVSHL 248
 Qy 138 QNQRRIIHRDMKPDNILLDEHGHVHITDFTNIAAMLPRETQITTMAGTKPYMAPEMSSRKG 197
 Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 249 HBRGIMERDLKPEENILMDTGHVMLTDGLAKEEFFENTRSNSMCGGTEYMAPBIV---RG 305
 Qy 198 AGYSEAVDWWSLGVTAYELLRGRPRPYHRSSTSSEEIVHTPFETTVVTVTPSAWSQEMVSLL 257
 Db 306 KGHDKAADWWSGILLYEMNLTKKPPFLGSKGKIQQKIV---KDOKIKLPQFLSNEAHAIL 361
 Qy 258 KKLLEPNPDR---FSQLSDVQNFQPYMNNDINWDAVFQKRLIIPGFIIPNKGRLNCDPTFE 312
 Db 362 KGLLQKEPERRLGSGLSGAEEBKQHKWFKGGINWKLEAREVMPSFKEPEVSGRCIANFD 420

RESULT 6

S37955 protein kinase YPK1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
 N;Alternate names: protein YKL126w
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Sep-1999
 C;Accession: S37955; A31248; S30903

R;Ramezani Rad, M.; Xu, G.; Kirchherr, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P.
 Submitted to the Protein Sequence Database, March 1994
 A;Reference number: S37953
 A;Accession: S37955
 A;Molecule type: DNA
 A;Cross-references: EMBL:Z28126; NID:9486212; PIDN:CAA81967.1; PID:g486213; MIPS:YKL12
 A;Experimental source: strain S288C
 R;Maurer, R.A.
 DNA 7, 469-474, 1988
 A;Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein
 A;Reference number: A31248; MUID:89090805; PMID:2850145
 A;Accession: A31248
 A;Molecule type: DNA
 A;Residues: 1-200, 'L', 202-552, 'I', 554-680 <MAU>
 A;Cross-references: EMBL:M21307; NID:g172180; PIDN:AAA34880.1; PID:g172181
 R;Chen, P.; Lee, K.S.; Levin, D.E.
 Mol. Gen. Genet. 236, 443-447, 1993
 A;Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell
 A;Reference number: S30903; MUID:93173125; PMID:8437590
 A;Accession: S30903
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-200, 'L', 202-226, 'T', 228-552, 'I', 554-680 <CHE>
 C;Genetics:
 A;Gene: SGD:YPK1
 A;Cross-references: SGD:S0001609; MIPS:YKL126w
 A;Map position: 11L
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homo
 C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 P;345-602/Domain: protein kinase ATP-binding motif
 F;353-361/Region: protein kinase ATP-binding motif
 F;470/Active site: Asp #status predicted

Query Match 24.4%; Score 513; DB 2; Length 680;
 Best Local Similarity 32.0%; Pred. No. 3.8e-16;
 Matches 115; Conservative 78; Mismatches 124; Indels 42; Gaps 10;

Qy 8 KPPVFDENEVDNFDFEILRAIGKGSFGEYCVIQKNNDTKKMCAMKYMNNKKQKCVERNEVTRN 67
 Db 335 KP---SRNKPLSIDDFDLKVIGKGSFGKVMQVRKKDTOKVAKAIRKSYIVSKSEVTH 391

Qy 68 VPKBLQIMQGLEBHPFLVNLWYSFQDDEDMFMVVDLILGGDLRYHLQQNQVHFKEETVLF 127
 Db 392 TLAERTVLAIRDVDCPFIVPLKFQSPOSPEKLYFVLAFINGGELFYHLQKEGRFDLSRARFT 451

Qy 128 CBLVMALDYLQNQRRIIHRDMKPDNILLDEHGHVHITDFTNIAAMLPRETQIT-TMAGTKPY 186
 Db 452 ARLLCALDNLHKLDDVYRDILKEENILLDQYQHIALCDFGLCKLMKDDDKTDTFCGTPFV 511

Qy 187 MAPEMFSRKGAGYSFAVDWWSLGVTAYELLRGRPRPYHRSSTSSEEIVHTPFETTV---V 243
 Db 512 LAPELL--LGLGYTKAVDWWTGLVLLYEMLTGLPPYY-----DEDVPKMYKKJLQEPL 562

Qy 244 TYPSAWSQEMVSLLKKLBPNDQR--FSQLSDVQNFQPYMNDINWDVQRKLIPGFIPI 301
 Db 563 VPPDGFDRAKDLIGLLSRDETRRLGYNGADEIRNHPFFSQLSWKRLMKGYIPPYKPA 622

Qy 302 KGRLNCDPTEELLEMILESKPLHKKKKRKLAKKEKDKMRKCDSSQTCILLOEHL-DSVQKEF 359
 Db 623 VS--NSMDTSNFDEEFTRBKPI-----DS---VVDEYLSSESVQKQP 658

RESULT 7

S55694 protein kinase (EC 2.7.1.37) sck1, cAMP-dependent - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe*
 C;Accession: S55694; T38040
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Nov-2000
 R;Jin, M.; Fujita, M.; Culley, B.M.; Apolinario, B.; Yamamoto, M.; Maundrell, K.; Hoff
 Genetics 140, 457-467, 1995
 A;Title: sck1, a high copy number suppressor of defects in the cAMP-dependent protein
 A;Reference number: S55694; MUID:96120227; PMID:7498728

A; Accession: S55694
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-696 <JIN>
 A; Cross-references: GB:D38108; NID:g1136301; PIDN:BAA07286.1; PID:d1007864; PID:g1136302
 A; Note: the authors translated the codon GAT for residue 687 as His
 R; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, C.M.
 Submitted to the EMBL Data Library, August 1999
 A; Reference number: Z21764
 A; Accession: T38040
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-176, 'F', 178-198, 'A', 200-696 <MCID>
 A; Cross-references: EMBL:AL109951; PIDN:CAB53053.1; GSPDB:GN00066; SPDB:SPAC1B9.02C
 A; Experimental source: strain 972h-; cosmid c1B9
 C; Genetics:
 A; Gene: sck1; SPDB:SPAC1B9.02C
 A; Map position: 1
 A; Introns: 80/3; 311/1; 633/2
 C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C; Keywords: ATP; phosphotransferase; protein kinase
 F; 300-563/Domain: protein kinase homology <KIN>
 F; 308-316/Region: protein kinase ATP-binding motif

Query	Match	Score	Length
Qy	24.38; Best Local Similarity 36.9%; Pred. No. 4.5e-16; Matches 111; Conservative 63; Mismatches 112; Indels 15; Gaps 7;	511.5	696;
Db	11 VFDENEDVNPF--DHFPEILRAIGKGGSFGEVCIVQKNDTAKMCKYMNKQKCVERNEVRNNV 68		
Qy	69 FKELOQIMQGL--EHPFLVNLWYSFQDEEDMFMVVDLILLGGDLRYHLQQNVLHFKETTVKL 125		
Db	288 IYEHIEHVRYGPEDFTALRLIGKGTFGQQVYLVLRKNDTNRUYAMKKKISKKLIVRKKEVTHT 347		
Qy	126 FICELVMLADYLQNQRRIIHRDMKPDNVLLDEGHVHITDFNIA-AMLPREQITTMAGTK 184		
Db	408 YIAELVLALEHLHKHDIIYRDLKOPENVILLDAKGHALCDFGLSKANLSANATNTPCGTT 467		
Qy	185 PYMAPEMFSSRKGAGGYSFAVDWWSLGVTAYELLGRGRPYHIRSSTSSEIVHTPETTVVT 244		
Db	468 EYLAPEVLLEDK--GYTKQVDFWSLGVLVPEMCCGWSPPFY--APDVQQMVRNIAFGKVR 522		
Qy	245 YP-SAWSQEMVSLLKKLLEPNPDQRFSQLSD---VQNPFPYMDINWDVFQKRLLIPGFIP 300		
Db	523 FPKGVLSSEGRSFVRGLINRNPNHRLGAVADTTTELKEHPPFFADINWDLSSLKKVQPPFKP 582		
Qy	301 N 301		
Db	583 N 583		

RESULT 8

C31751 protein kinase (EC 2.7.1.37), cAMP-dependent, catalytic chain - fruit fly (Drosophila melanogaster)
 C; Species: Drosophila melanogaster
 C; Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1999
 C; Accession: C31751; A28269
 R; Kalderon, D.; Rubin, G.M.
Genes Dev. 2, 1539-1556, 1988
 A; Title: Isolation and characterization of Drosophila cAMP-dependent protein kinase gene
 A; Reference number: A31751; MUID:89107990; PMID:3215511
 A; Accession: C31751
 A; Molecule type: DNA
 A; Residues: 1-353 <KAL>
 A; Cross-references: EMBL:X16969; NID:g7806; PIDN:CAA34840.1; PID:g7807; EMBL:Y00220
 R; Foster, J.L.; Higgins, G.C.; Jackson, P.R.
J. Biol. Chem. 263, 1676-1681, 1988
 A; Title: Cloning, sequence, and expression of the Drosophila cAMP-dependent protein kinase
 A; Reference number: A92684; MUID:88115281; PMID:2828348
 A; Accession: A28269
 A; Molecule type: DNA

Db	116 FSGNDDTSEKSPEEVSGVVGIEDFEVLLKTVVGQAGFGKVYQVRKKOTSEIYAMKVMRKDK 175	RESULT 11
Qy	59 CVERNEVRNVFKELQIMQGLEHPPFLVNLWYSFQDDEEDMFMVVDLLGGDLRYHLQQNQVHP 118	T20232 hypothetical protein C54G4.1 - Caenorhabditis elegans
Db	176 IVEKNHAEMYKAERDILTKIDHPPFIVQLKYSFQTKYRLVLDFINGGHLLFQLYHOGLF 235	C;Species: Caenorhabditis elegans
Qy	119 KEETVKLPICELVMALDYLQNORIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQIT 178	C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
Db	236 REDLARYVTAEIVSVVSHLHERGIMHRDLKPENILMDVDGHVMIITDFGLAKEFEENTRSN 295	C;Accession: T20232 R;Wilkinson, J.
Qy	179 TMAGTKPYPMAPEMFSSRKCGAGYSFAVDWWSLGVTTAYELLRGRPYHIRSTSSKBIYHTF 238	submitted to the EMBL Data Library, June 1996
Db	296 SMCGTTEYMAPEIV--RGKGHDKAADWWSGVILLYEMLTGKPPFLGSKGKIQQQKIV--- 349	A;Accession: T20232 A;Status: preliminary; translated from GB/EMBL/DDBJ
Qy	239 ETTVVTPPSAWSQEMVSLLKCLLEPNPQDFR---SOLSDVQNPYIMNDINWDAVFQKRL 294	A;Molecule type: DNA
Db	350 -KDKIKLPPQFVFNEAHALLKGGLLQKEPERRRLGSGPSGAEEIKHHWKFKAINWKKLEARREV 408	A;Residues: 1-785 <WIL>
Qy	295 IPGIPNKGRLNCDPTFB 312	A;Cross-references: EMBL:275533; PIDN:CAA99814.1; GSPDB:GN00019; CESP:C54G4.1
Db	409 QPSFKPAVSGRQCIANFD 426	A;Experimental source: clone C54G4
Qy	24.1%; Score 506.5; DB 2; Length 785;	A;Map position: 1
Db	A;Introns: 55/3; 188/2; 237/2; 339/3; 397/2; 474/3; 504/3; 558/2; 594/3; 687/1; 736/2	C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
Qy	24.1%; Score 506.5; DB 2; Length 785;	C;Genetics:
Db	A;Best Local Similarity 36.3%; Pred. No. 8.4e-16; Matches 109; Conservative 73; Mismatches 107; Indels 11; Gaps 8;	A;Map position: 1
Qy	14 ENEDVNFDHFPEILRAIGKGSFGEVCIYQK---NDTKMKCAMKYMNKQKCVERNE-VRNTYF 69	A;Intros: 55/3; 188/2; 237/2; 339/3; 397/2; 474/3; 504/3; 558/2; 594/3; 687/1; 736/2
Db	8 EGKEVKSMEFNALLRVLGKGAYGKRVFLYRKVGKDHNTIYAMKVLRKTRVLTKQTLEHTM 67	C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
Qy	70 KELQIMQGLE-HPFVLNLWYSFQDDEEDMFMVV DLLGGDLRYHLQQNQVHFEETVKLPLIC 128	A;Map position: 1
Db	68 ABRQVLERLRLRGTPPFVLNLFYAFQTDTRKLVHIVMEYVRGGELFTLCSRGHFDFLEAARFVIA 127	C;Genetics:
Qy	129 BLVMAVDYLNQRIIHDMKPDNILLDEGHVHITDENIAAM-LPRE-TQITTMAGTKPY 186	A;Map position: 1
Db	128 ELVVAIDSLLHQRKVITYRDLKLENILLLDEGHVHLKTDFGLSKLFLPGELDRANSYCGTIEY 187	C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
Qy	187 MAPEMFSSRKCGAGYSFAVDWWSLGVTTAYELLRGRPYHI-RSSTSSKKEIVHTFETTVVTY 245	A;Map position: 1
Db	188 MSPEVINRPEG-GYSDVDDWWSLGVTLSEFLLTGCSPEFTVDAQNSSSKDIAKRIMTRCKVPPF 246	C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
Qy	246 PSAWSQBMVSLLKCLLBPNPQDFR--FSQLSDVQNPYMNNDINWDAVFQKRLIPGPIPNKG 303	A;Map position: 1
Db	247 PKTMDVDARDFIGQQLLEKKLEKRLGYNGVDEIKNHKEMSSIDWDAAVKRTLKPVIVPRIG 306	C;Genetics:
Qy	24.1%; Score 507; DB 2; Length 352;	A;Map position: 1
Db	A;Best Local Similarity 33.3%; Pred. No. 4e-16; Matches 108; Conservative 82; Mismatches 104; Indels 30; Gaps 10;	RESULT 12
Qy	21 DHFBEILRAIGKGSFGEVCIYQ-KNDTKMKCAMKYMNKQKCVERNEVRNFVKELQIMQGLE 79	T21211 hypothetical protein ZK909.2a - Caenorhabditis elegans
Db	42 DDFDRIKTLGTGSFGRVMLYQHKGESRNFYAMKILDQKVVKLKOVENTLNEKKILQSIN 101	C;Species: Caenorhabditis elegans
Qy	80 HPFLVNLWYSFQDDEEDMFMVV DLLGGDLRYHLQQNQVHFEETVKLPLICELVMAVDYLNQ 139	C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
Db	102 FPFLVNLLEYSFQDNNSNLYMVKLEFTVTTGEMFSHLRIGRFSEFHRSRFYAAQIVLVEYHH 161	C;Accession: T21211; T28100
Qy	140 QRIIHDMKPDNILLDEGHVHITDENIAAMLPRETQITTMAGTKPYMAPEMFSSRKGAG 199	R;McClay, K.
Db	162 LDIMYRDLKPENNLLIDSYGYLKVTDFGFAKRVKGRT--WTLCTGTPPEYLAPETILSK---G 216	A;Status: preliminary; translated from GB/EMBL/DDBJ
Qy	200 YSPAVDWWSLGVTTAYELLRGRPYHIRSTSSKEIVHTFETTV---VTVTPSAWSQEMVSL 256	A;Molecule type: DNA
Db	217 YNKAVIDWWALGVLIYEMAAGYPPFF----ADQPIQIYEKIVSGKVRFPSHFSSDLKDL 270	A;Residues: 1-359 <WIL>
Qy	257 LKKLLEPNPQDFRSQL---SDVQNPYMNNDINWDAVFQKRLIPGPPIP-NKGRLNCDFTF 311	A;Accession: T28100
Db	271 LRNLQVDLTKRFGNLKNGNDIXNKHWPSTTDWAIYQRKVEAPFVPKTKG--AGDTA 327	A;Status: preliminary; translated from GB/EMBL/DDBJ
Qy	312 ELEMILESKPLHKKKKRKLAKKEK 335	A;Molecule type: DNA
Db	328 NFDD-YEEEPL---RISSTEK 344	A;Residues: 1-359 <WIL>

A;Introns: 24/1; 44/3; 87/3; 120/3; 190/3; 318/3
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 24.0%; Score 506; DB 2; Length 359;
Best Local Similarity 33.0%; Pred. No. 4.5e-16;
Matches 109; Conservative 78; Mismatches 121; Indels 22; Gaps 7;

Qy 14 ENEDVN---FDHPEILRAIGKGSFGEVCIQKNDTKMCAKYMNKQKCVERNEVRNVFK 70
Db 40 ENPAQNTACLDDFDIRKTLGTGSFGRVMLYKHKKGNSGNYYAMKILDKQKVVKLQKVETHTLN 99
Qy 71 ELQIMQGLEHPPFLVNLWYSFQDEEDMFMVVDLLGGDLRYHQVNHFKEETVKLFICEL 130
Db 100 ECRILQAIDFPFLVNMTEFSPKDNSNLYMVLREFISGGEMFSHLRRIGRSEPHSRFYAAQI 159
Qy 131 VMALDYLQNQRRIHRDMCKPDNILLDEGHVHITDFNIAAMLPRETOITTMAGTKPYPEAPE 190
Db 160 VLAPEYLHSDLIYRDLKPENLLIDSTGKRTDFGFAKRVKGRT--WTLCGTPBEYLAPE 217

RESULT 14
OKHYCA

191 MFSSRKKGAGYSFAVDWWSLGVTAYELLRGGRPYHRSSTSKEIVHTFBETTV---VTYPS 247
Db 218 IILSK---GYNKAVIDWALGVLIYEMAAGYPPFF-----ADQPIQIYEKIVSGKVKFPPS 268

Qy 248 AWSQEMVSLLKKLLEPNPDPQRFSQL---SDVQNFPYMNDDAVFQKRLLPGFIPN-K 302
Db 269 HPSNELKLKLNLLQVDTLKRYGNLNGVADIKNHKWFGSTDWIAIYQKKTIPPPSP-SKG 327

Qy 303 GRLNCDDPTFELLEMILESKPLHKKKKKKRLLAK 332
Db 329 GPGDASNPDDYEEPLRISGTETKCAKEPFAE 358

RESULT 13
T21212

hypothetical protein ZK909.2b - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Accession: T21212; T28101
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
R;McClay, K.
Submitted to the ENBL Data Library, November 1996
A;Reference number: Z19391
A;Accession: T21212
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-375 <WIL>
A;Cross-references: EMBL:Z81511; PIDN: CAB04169.1; GSPDB: GN00019; CESP: ZK909.2b
A;Experimental source: clone P21F12
R;White, S.
Submitted to the ENBL Data Library, November 1996
A;Reference number: Z20469
A;Accession: T28101
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-375 <WIL>
A;Cross-references: EMBL:Z822096; PIDN: CAB05035.1; GSPDB: GN00019; CESP: ZK909.2b
A;Gene: CESP:ZK909.2b
A;Map position: 1
A;Introns: 24/1; 44/3; 87/3; 120/3; 190/3; 318/3
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 23.9%; Score 503; DB 2; Length 375;
Best Local Similarity 34.3%; Pred. No. 6.3e-16;
Matches 104; Conservative 74; Mismatches 103; Indels 22; Gaps 7;

Query Match 23.9%; Score 503; DB 2; Length 375;
Best Local Similarity 34.3%; Pred. No. 6.3e-16;
Matches 104; Conservative 74; Mismatches 103; Indels 22; Gaps 7;

Qy 14 ENEDVN---FDHPEILRAIGKGSFGEVCIQKNDTKMCAKYMNKQKCVERNEVRNVFK 70
Db 40 ENPAQNTACLDDFDIRKTLGTGSFGRVMLYKHKKGNSGNYAMKILDQKVVKLQKVETHTLN 99

Qy 71 ELQIMQGLEHPPFLVNLWYSFQDEEDMFMVVDLLGGDLRYHQVNHFKEETVKLFICEL 130
Db 100 ECRILQAIDFPFLVNMTEFSPKDNSNLYMVLREFISGGEMFSHLRRIGRSEPHSRFYAAQI 159

Qy 131 VMALDYLQNQRRIHRDMCKPDNILLDEGHVHITDFNIAAMLPRETOITTMAGTKPYPEAPE 190
Db 160 VLAPEYLHSDLIYRDLKPENLLIDSTGKRT--WTLCGTPBEYLAPE 217
Qy 191 MFSSRKKGAGYSFAVDWWSLGVTAYELLRGGRPYHRSSTSKEIVHTFBETTV---VTYPS 247
Db 218 IILSK---GYNKAVIDWALGVLIYEMAAGYPPFF-----ADQPIQIYEKIVSGKVKFPPS 268
Qy 248 AWSQEMVSLLKKLLEPNPDPQRFSQL---SDVQNFPYMNDDAVFQKRLLPGFIPNKG 303
Db 269 HPSNELKLKLNLLQVDTLKRYGNLNGVADIKNHKWFGSTDWIAIYQKKTIPPPSP-SKG 327
Qy 304 RLN 306
Db 328 ESN 330

RESULT 14
OKHYCA
protein kinase (EC 2.7.1.37), cAMP-dependent, alpha catalytic chain - Chinese hamster
C;Species: Cricetulus griseus (Chine  se hamster)
C;Date: 31-Dec-1993 #sequence_revision 31-Jun-1999
C;Accession: B40384
R;Howard, P.; Day, K.H.; Kim, K.B.; Richardson, J.; Abraham, I.; Fleischm.
J. Biol. Chem. 266, 10189-10195, 1991
A;Title: Decreased catalytic subunit mRNA levels and altered catalytic subunit mRNA si
A;Reference number: A40384; PMID: 91244783; PMID: 1645343
A;Accession: B40384
A;Molecule type: mRNA
A;Residues: 1-351 <HOW>
A;Cross-references: GB: M63311; NID: 9191174; PIDN: AAA37010.1; PMID: 9191175
C;Comment: The inactive enzyme contains two regulatory chains and two catalytic chain
C;Two types found in mammalian tissue are distinguished by having either type I or type II
C;Comment: Both alpha and beta catalytic chains are found in many tissues, with the a
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; blocked amino end; cAMP binding; heterotetramer; lipoprotein; magnes
P;2-351/Product: protein kinase, cAMP-dependent, alpha catalytic chain #status predicted
P;42-298/Domain: protein kinase homology <KIN>
P;50-58/Region: protein ATP-binding motif
P;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
P;3/Modified site: aspartic acid (Asn) #status predicted
P;11, 339/Binding site: phosphate (Ser) (covalent)
P;55, 56, 122, 128, 171, 184/Binding site: Mg-ATP (Phe, Gly, Glu, Glu, Glu, Thr) #status p
P;73, 92, 167, 169/Active site: Lys, Glu, Asp, Lys #status predicted
P;172, 185/Binding site: magnesium (Asn, Asp) #status predicted
P;198/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 23.9%; Score 502.5; DB 1; Length 351;
Best Local Similarity 34.0%; Pred. No. 6.2e-16;
Matches 99; Conservative 76; Mismatches 97; Indels 19; Gaps 6;

Qy 21 DHFBDIILGKGSFGBEVCIQVQNDTKMCAKYMNKQKCVERNEVRNVFKELQIMQGLEH 80
Db 42 DHFDRIKTLGTSFGRVMLVXHKETGNHYAMKILDKOKVVKLQKQIENTLNKRILQAVNF 101
Qy 81 PFLVNLWYSFODEEDMFMVVDLLGGDLRYHQVNHFKEETVKLFICELMADLYLQNQ 140
Db 102 PFLVKELEFSPKDNNSLYMVEYVPGGEMFSHLRRIGRSEPHARFYAAQIVLTPEYLHSL 161
Qy 141 RIHRDMCKPDNILLDEGHVHITDFNIAAMLPRETOITTMAGTKPYPEAPESSRKKGAGY 200
Db 162 DLYRDLKPENLLIDQQGYIQVTDGFAGAKRVKGRT--WTLCGTPBEYLPEILSK--GY 216
Qy 201 SFAVDWWSLGVTAYELLRGGRPYHRSSTSKEIVHTFBETTV---VTYPSAWSQEMVSLL 257
Db 217 NKAVDWWALGVLIYEMAAGYPPFF-----ADQPIQIYEKIVSGKVRFPSSHSSDLKQLL 270
Qy 258 KKLBEPNPDQRFSQL---SDVQNFPYMNDDAVFQKRLLPGFIPN-KG 303
Db 271 RNLLQVDLIXRFGNLKAGVNDIANKHWFATTDWIAIYQKKTIPPPSP-SKG 321

Search completed: June 25, 2004, 10:50:09
 Job time : 22 SECS

RESULT 15

S48986 probable protein kinase SCH9 (EC 2.7.1.-) - yeast (saccharomyces cerevisiae)

N;Alternate names: protein YHR205w

C;Species: Saccharomyces cerevisiae

C;Date: 02-Dec-1994 #Sequence revision 02-Dec-1994 #text_change 24-Sep-1999

C;Accession: S48986; S30022; A28429

R;Macri, C.

submitted to the EMBL Data Library, February 1994

A;Description: The sequence of S. cerevisiae cosmid 9177.

A;Reference number: S46671

A;Accession: S48986

A;Molecule type: DNA

A;Residues: 1-823 <MAC>

A;Cross-references: EMBL:U00029; NID:g551322; PIDN:AAB69735.1; PID:g458923; MIPS:YHR205w

A;Cross-references: EMBL:X57629; NID:g5277; PIDN:CAA40853.1; PID:g5279

A;Note: The nucleotide sequence was submitted to the EMBL Data Library, February 1991

R;Toda, T.; Cameron, S.; Sasse, P.; Wigler, M.

Genes Dev. 2, 517-527, 1988

A;Title: SCH9, a gene of Saccharomyces cerevisiae that encodes a protein distinct from,

A;Reference number: A28429; MUID:88255839; PMID:3290050

A;Accession: A28429

A;Molecule type: DNA

A;Residues: 'M', 1-364, 'S', 366-749, 'K', 751-823 <TOD>

A;Cross-references: EMBL:X12560; NID:g4425; PIDN:CAA31073.1; PID:g4426

C;Genetics:

A;Gene: SGD:SCH9

A;Cross-references: SGD:S0001248; MIPS:YHR205w

A;Map position: 8R

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

P;409-670/Domain: protein kinase homology <KIN>

F;417-425/Region: protein kinase ATP-binding motif

A;Genetics:

A;Cross-references: SGD:S0001248; MIPS:YHR205w

A;Map position: 8R

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

P;409-670/Domain: protein kinase homology <KIN>

F;417-425/Region: protein kinase ATP-binding motif

Query Match 23.9%; Score 502.5; DB 2; Length 823;
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 Db 378 SLKPRVIDEVVSGDILIKWTKYQTRKKRHYPQDFEYVLLGKTFGQvYQVKKQDTQRIY 4.37Qy 50 AMKYMNKQKCVERNEVRNPVKELQIM--QGLEHPFLVNLWYSQDDEDMFMVVDLILLGG 1.06
 Db 438 AMKVLSKKRVIVCKNEIAHTIGERNILYTAKSSSPFTVGLKFSQFTPTDLYLTDMMSG 4.97Qy 107 DLRYHLQQNVHFKKEETVKLPICELVMALDYLQNQRIIHRDMKPDNILLDEBHGIVHITDFN 1.66
 Db 498 ELFWHLOKEGRPSEDRAKFYIAELVLALEHLHDNDIYVRLDKPENILLDANGNIALCDFG 5.57Qy 167 IA-AMLPRETQITTMAGTKPVMAPEMSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHI 2.25
 Db 558 LSKADLKDRT--NTFCGTTEYLAPELLDE-TGYTRKMDFWSLGVLIPEMCCGWSPEFF- 6.12Qy 226 RSSTSSKEIVHTPFTTETTVVTYTP-SAWSQEMVSLLKKLLEPQLNPDQRFSQLSD--VQNFPM 2.81
 Db 613 --AENNQKMYQKIAFGKVKPRDVLSQEGRSFVKGLLNRNPKHRLGAIDDGRELRAHPFP 6.70Qy 282 NDINWDADVQKRLIPGFIPN----KGRLNCDFP 3.11
 Db 671 ADIDWEALKQKCKIPPPFKPHLVSETDSNFDPEP 7.04

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2004, 10:50:15 ; Search time 48 Seconds
 (without alignments)
 2329.088 Million cell updates/sec

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 Perfect score: 2104
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Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	2104	100.0	396	US-10-667-442-2
3	2104	100.0	396	US-10-254-869-2
4	2089	99.3	396	US-09-841-683-11
5	2089	99.3	396	US-10-362-892-20
6	2089	99.3	396	US-10-182-243-33
7	2089	99.3	396	US-10-288-798-20
8	2083	99.0	396	US-10-410-764-101
9	2047	97.3	407	US-09-841-683-9
10	1814	86.2	358	US-10-108-260-2674
11	1437.5	68.3	414	US-10-074-978A-158
12	1427	67.8	404	US-09-801-876B-4
13	1427	67.8	404	US-10-667-442-4
14	1427	67.8	404	US-10-254-869-4
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16	1425.5	67.8	403	US-10-667-442-5
17	1425.5	67.8	403	US-10-254-869-5
18	1425.5	67.8	414	US-10-354-358-36
19	1425.5	67.8	414	US-10-074-978A-157
20	1324	62.9	419	US-09-799-875-14
21	1324	62.9	419	US-10-649-156-14
22	1324	62.9	419	US-10-303-664A-6
23	1318	62.6	485	US-10-415-011-12
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28	1302	61.9	488	US-10-074-978A-18
29	1278.5	60.8	399	US-09-819-607-4
30	1278.5	60.8	399	US-10-633-631-4
31	1259.5	59.9	375	US-10-168-582-12
32	1201.5	57.1	364	US-10-206-915-572
33	1201.5	57.1	364	US-10-199-670-572
34	1201.5	57.1	364	US-10-201-858-572
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39	1201.5	57.1	364	US-10-176-483-572
40	1201.5	57.1	364	US-10-176-749-572
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45	1201.5	57.1	364	US-10-183-014-572

ALIGNMENTS

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RESULT 1
; Sequence 2, Application US/09801876B
; Patent No. US20020127683A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-09-801-876B-2
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Query Match Best Local Similarity	Score 100.0%	DB 9;	Length 396;	
Matches 396;	Pred. No. 5e-169;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 MGANTSRKPPFVFDENEDVNFIQLKIGKGSFGEVCIYQNDTKMCKMCKYMKQKCV	60		
Db	1 MGANTSRKPPFVFDENEDVNFIQLKIGKGSFGEVCIYQNDTKMCKMCKYMKQKCV	60		
Qy	1 ERNEVRNVFKELQIMQGLEHFPFLVNLWYSFQDEEDMFMVVDLGGDLRYHLQQNHFKB	120		
Db	1 ERNEVRNVFKELQIMQGLEHFPFLVNLWYSFQDEEDMFMVVDLGGDLRYHLQQNHFKB	120		
Qy	1 AGTKPMPAMPEMFSSRKGAGYSFAYDWWSLGTVAYELLRGRPRYHRSSTSKEIVHTFET	240		
Db	1 ETVKLFICELVMALDDYLQNORIITHRDMDKPDNILLDEHGHVHTDFNIAAMLPRETQITTM	180		
Qy	1 ETVKLFICELVMALDDYLQNORIITHRDMDKPDNILLDEHGHVHTDFNIAAMLPRETQITTM	180		

obj	181	AGTKPMAPEMFSSRKGAGYSPAVDWTLGVTTAYELLRGRRPYHRSSTSKEIVHTPET	240
Qy	241	TVVVTPSAWSQEMVSLLKKLLEPNPDQRPSQLSDVQNFPYMNDINWDAVFQKRLIPGFI P	300
obj	241	TVVVTPSAWSQEMVSLLKKLLEPNPDQRPSQLSDVQNFPYMNDINWDAVFQKRLIPGFI P	300
Qy	301	NKGRLNCDPTFPELEEMILESKPLHKKKRLLAKCEKDMRKCDSSQTCLIQEHLDSVQKEFI	360
obj	301	NKGRLNCDPTFPELEEMILESKPLHKKKRLLAKCEKDMRKCDSSQTCLIQEHLDSVQKEFI	360
Qy	361	IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL	396
obj	361	IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL	396

RESULT 2
US-10-667-442-2 ; Sequence 2, Application US/10667442
; Publication No. US20040043466A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USBS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV II
; CURRENT APPLICATION NUMBER: US/10/667,442
; CURRENT FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-667-442-2

Query Match 100.0%; Score 2104; DB 12; Length 396;
 Best Local Similarity 100.0%; Pred. No. 5e-169;
 Matches 396; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

1	MGANTSRKPPVFDENEDVNPDHF <small>b</small>	ILRAIGKGSFGEV CIVQKNTDKCMCAMKCYMANKQKCV	60
1	MGANTSRKPPVFDENEDVNPDHF <small>b</small>	ILRAIGKGSFGEV CIVQKNTDKCMCAMKCYMANKQKCV	60
61	ERNEVRNVFKELQIMQGLEHPPFLVNWLWYSPQDEEDDMFMVVDLLIGGDLRYHLQQMVHFKE	120	
61	ERNEVRNVFKELQIMQGLEHPPFLVNWLWYSPQDEEDDMFMVVDLLIGGDLRYHLQQMVHFKE	120	

Qy	181	AGTKP ^Y MAPEMFSSRKGAGYSFAVDW ^W SLGVTA ^Y ELLRG ^R RPYH ^R S ^T SSKEI ^V H ^T PET	240
Db	181	AGTKP ^Y MAPEMFSSRKGAGYSFAVDW ^W SLGVTA ^Y ELLRG ^R RPYH ^R S ^T SSKEI ^V H ^T FET	240
Qy	241	TVV ^T YPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKR ^L I ^P G ^F IP	300
Db	241	TVV ^T YPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNDINWDAVFQKR ^L I ^P G ^F IP	300
Qy	301	NKGR ^L NCDP ^T FELEEMILES ^K PLH ^K CK ^K RLAK ^E K ^D M ^R KCDS ^S QTCLLQE ^H LD ^S VQ ^K E ^P I	360
Db	301	NKGR ^L NCDP ^T FELEEMILES ^K PLH ^K CK ^K RLAK ^E K ^D M ^R KCDS ^S QTCLLQE ^H LD ^S VQ ^K E ^F I	360
Qy	361	I ^F NREKVNRDENKROPNLALEQTKDPOQGEDGQNNNL	396
Db	361	I ^F NREKVNRDENKROPNLALEBOTTKDPOGEDGQNNNL	396

RESULT 3
US-10-254-869-2 ; Sequence 2, Application US/10254869
; Publication No. US20030027307A1 ; GENERAL INFORMATION

APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
TITLE OF INVENTION:
FILE REFERENCE: CL001160DIV
CURRENT APPLICATION NUMBER: US/10/254,869
CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ For Windows Version 4.0
SEQ ID NO 2
LENGTH: 396
TYPE: PRT
ORGANISM: Human
US-10-254-869-2

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Query Match          100.0%; Score 2104; DB 14; Length 396;
Best Local Similarity 100.0%; Pred. No. 5e-169;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MGANTSRKPPVFDENEDVNFDHEIILRAIGKGSFGEVCIVQKNDTICMAMCYSNNKQKCV 60
       1 MGANTSRKPPVFDENEDVNFDHEIILRAIGKGSFGEVCIVQKNDTICMAMCYSNNKQKCV 60

Db      61 ERNEVRNVPKELQIMQGLEHPFLVNLWYSFQDEEDDMFMVVDLLGGDLRYHLQQNVHFKE 120
       61 ERNEVRNVPKELQIMQGLEHPFLVNLWYSFQDEEDDMFMVVDLLGGDLRYHLQQNVHFKE 120

Qy      121 STVVKLFPICELVMALDYLQNQRRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
       121 STVVKLFPICELVMALDYLQNQRRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180

Db      181 AGTKPYNMAPEMFSSRKGAGYSPAVDWWSLGVVTAYBLLRGRRPYHIRSSTTSKKBVHTFBT 240
       181 AGTKPYNMAPEMFSSRKGAGYSPAVDWWSLGVVTAYBLLRGRRPYHIRSSTTSKKBVHTFBT 240

Qy      241 TTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNIDINWDAVFQKRLLPGFIP 300
       241 TTVVTYPSAWSQEMVSLLKKLLEPNPDQRFSQLSDVQNFPYMNIDINWDAVFQKRLLPGFIP 300

Db      301 NKGRLNCDPTPELEEMILESKPLHKKKRKLAKKEKDMRKCDSSQTCLLQEHLDSVQKBFPI 360
       301 NKGRLNCDPTPELEEMILESKPLHKKKRKLAKKEKDMRKCDSSQTCLLQEHLDSVQKBFPI 360

Qy      361 IFNREKVNRDFNKQOPNLALEQTKDpqgedgqnnnl 396
       361 IFNREKVNRDFNKQOPNLALEQTKDpqgedgqnnnl 396

Db      .. .

```

RESULT 4
US-09-841-683-11
Sequence 11, Application US/09841683
Patent No. US20020081600A1
GENERAL INFORMATION:
APPLICANT: Hu, Yi
APPLICANT: Nepomnichy, Boris
APPLICANT: Wang, Xiaoming
APPLICANT: Donoho, Gregory
APPLICANT: Scoville, John
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: NO. US20020081600A1el Human Kinase Proteins and Polynucleotides
FILE REFERENCE: LEX-0167-USA
CURRENT APPLICATION NUMBER: US/09/841,683
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 60/199,499
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 60/201,227
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11

US-09-841-683-11

Query Match 99.3%; Score 2089; DB 9; Length 396;
Best Local Similarity 99.5%; Pred. No. 9.3e-168;
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMCKMNQKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCAMCKMNQKCV 60

Qy 61 ERNEVRNVPKELQIMOGLEHPFLVNLWYSFQDEEDDMFMVVDLILGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVPKELQIMOGLEHPFLVNLWYSFQDEEDDMFMVVDLILGGDLRYHLQONVHFKE 120

Qy 121 ETVKLIFICBLVMAVDLYLQNORIIRDMKPDNILLDEHGHVHTIDFNIAAMLPREQTITM 180
Db 121 ETVKLIFICBLVMAVDLYLQNORIIRDMKPDNILLDEHGHVHTIDFNIAAMLPREQTITM 180

Qy 181 AGTKPYPMAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSKEIVHTFET 240
Db 181 AGTKPYPMAPEMFSSRKGAGYSFAVDWWSLGVTAYELLRGRRPYHIRSSTSKEIVHTFET 240

Qy 241 TVVTPYPSAWSQEMVSLLKKLLEPDKRPSQDSVQNFPMNDINWDAVQKRLLPGFIP 300
Db 241 TVVTPYPSAWSQEMVSLLKKLLEPDKRPSQDSVQNFPMNDINWDAVQKRLLPGFIP 300

Qy 301 NKGRINCDPTFELLEMILESKPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHLDSVQKEFI 360
Db 301 NKGRINCDPTFELLEMILESKPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRFNKRQPNLAEQTKDPOGEDQNNNL 396
Db 361 IFNREKVNRFNKRQPNLAEQTKDPOGEDQNNNL 396

RESULT 5
US-10-362-892-20
; Publication No. US20040038881A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga
; APPLICANT: NGUYEN, Daniel B.; WALIA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: GANDHI, Ameena R.; GURUJAN, Rajagopal
; APPLICANT: DING, Li; PATTERSON, Chandra S.
; APPLICANT: YOB, Henry; BAUGHN, Mariah R.
; APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.
; APPLICANT: ELLIOTT, Vicki S.; LU, Yan
; APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
; APPLICANT: LAL, Preeti G.; RAMKUMAR, Jayalaxmi
; APPLICANT: WARREN, Bridget A.; KEARNEY, Liam
; APPLICANT: POLICKY, Jennifer L.; THANGAVELU, Kavitha
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PF-0209 USN
; CURRENT APPLICATION NUMBER: US 10/362, 892
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229, 873
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/231, 357
; PRIOR APPLICATION NUMBER: US 60/232, 654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/234, 902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236, 499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238, 389

US-10-182-243-33
; Sequence 33, Application US/10182243
; Publication No. US20040048310A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHAD
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; FILE REFERENCE: 038602/1366
; CURRENT APPLICATION NUMBER: US/10/182, 243
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US01/02337
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-182-243-33

Query Match 99.3%; Score 2089; DB 12; Length 396;

Best Local Similarity 99.5%; Pred. No. 9.3e-168;
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDHPBILRAIGKGSFGEVICIVQNDTKOMCAYMKYNNQQKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDHPBILRAIGKGSFGEVICIVQNDTKOMCAYMKYNNQQKCV 60

Qy 61 ERNEVRNVPKELQIMQGLEHPPFLVNLWYSFQDDEDEDMFMVVDLILLGGDLRYHQNTHFKE 120
Db 61 ERNEVRNVPKELQIMQGLEHPPFLVNLWYSFQDDEDEDMFMVVDLILLGGDLRYHQNTHFKE 120

Qy 121 ETVKLFICELVALDYLQNORIIRDMKPDNILLDEHGHVHTDNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVALDYLQNORIIRDMKPDNILLDEHGHVHTDNIAAMLPRETQITTM 180

Qy 181 AGTPKPYMAPEMFSSRKGAGYSFAVDWLSLGVTAYELLGRPRPHIRSSTS SKBIVHTFET 240
Db 181 AGTPKPYMAPEMFSSRKGAGYSFAVDWLSLGVTAYELLGRPRPHIRSSTS SKBIVHTFET 240

Qy 241 TVVTYPSAWSQEMVSLLKKLLEPDPORSOLSDVQNFPYMDINWDAVFQKRLLIPGFIP 300
Db 241 TVVTYPSAWSQEMVSLLKKLLEPDPORSOLSDVQNFPYMDINWDAVFQKRLLIPGFIP 300

Qy 301 NKGRLNCDPTFELEMILESKPLHKKKKRLLAKKEKDMDRKCDSSQTCCLLQEHLDSVQKEFI 360
Db 301 NKGRLNCDPTFELEMILESKPLHKKKKRLLAKKEKDMDRKCDSSQTCCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396
Db 361 IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396

RESULT 7
US-10-288-798-20
; Sequence 20, Application US/10288798
; Publication No. US20030207299A1

; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Daniel B;
; APPLICANT: WALIA, Narinder K.; HAPALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUB, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOLEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA

CURRENT APPLICATION NUMBER: US/10/288-798
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: PCT/US01/27219
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/240,542
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/238,389
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/236,499
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/234,902
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/232,654
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US 60/231,357
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: US 60/229,873
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 48

SOFTWARE: PERL Program
SEQ ID NO 20
LENGTH: 396
TYPE: PRT
ORGANISM: HOMO sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030207299A1 7946584CD1
US-10-288-798-20

Query Match 99.3%; Score 2089; DB 15; Length 396;
Best Local Similarity 99.5%; Pred. No. 9.3e-168;
Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDHPBILRAIGKGSFGEVICIVQNDTKOMCAYMKYNNQQKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDHPBILRAIGKGSFGEVICIVQNDTKOMCAYMKYNNQQKCV 60

Qy 61 ERNEVRNVPKELQIMQGLEHPPFLVNLWYSFQDDEDEDMFMVVDLILLGGDLRYHQNTHFKE 120
Db 61 ERNEVRNVPKELQIMQGLEHPPFLVNLWYSFQDDEDEDMFMVVDLILLGGDLRYHQNTHFKE 120

Qy 121 ETVKLFICELVALDYLQNORIIRDMKPDNILLDEHGHVHTDNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVALDYLQNORIIRDMKPDNILLDEHGHVHTDNIAAMLPRETQITTM 180

Qy 181 AGTPKPYMAPEMFSSRKGAGYSFAVDWLSLGVTAYELLGRPRPHIRSSTS SKBIVHTFET 240
Db 181 AGTPKPYMAPEMFSSRKGAGYSFAVDWLSLGVTAYELLGRPRPHIRSSTS SKBIVHTFET 240

Qy 241 TVVTYPSAWSQEMVSLLKKLLEPDPORSOLSDVQNFPYMDINWDAVFQKRLLIPGFIP 300
Db 241 TVVTYPSAWSQEMVSLLKKLLEPDPORSOLSDVQNFPYMDINWDAVFQKRLLIPGFIP 300

Qy 301 NKGRLNCDPTFELEMILESKPLHKKKKRLLAKKEKDMDRKCDSSQTCCLLQEHLDSVQKEFI 360
Db 301 NKGRLNCDPTFELEMILESKPLHKKKKRLLAKKEKDMDRKCDSSQTCCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396
Db 361 IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396

RESULT 8
US-10-410-764-101
; Sequence 101, Application US/10410764
; Publication No. US20040005664A1

; GENERAL INFORMATION:
; APPLICANT: NKGRLNCDPTFELEMILESKPLHKKKKRLLAKKEKDMDRKCDSSQTCCLLQEHLDSVQKEFI 360
; APPLICANT: NKGRLNCDPTFELEMILESKPLHKKKKRLLAKKEKDMDRKCDSSQTCCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396
Db 361 IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396

Qy 301 NKGRLNCDPTFELEMILESKPLHKKKKRLLAKKEKDMDRKCDSSQTCCLLQEHLDSVQKEFI 300
Db 301 NKGRLNCDPTFELEMILESKPLHKKKKRLLAKKEKDMDRKCDSSQTCCLLQEHLDSVQKEFI 300

Qy 361 IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396
Db 361 IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396

RESULT 8
US-10-410-764-101
; Sequence 101, Application US/10410764
; Publication No. US20040005664A1

; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapellner-Libermann, Rosana
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Title of Invention: 26199, 33530, 33949, 47148, 50226,
; APPLICANT: Prior Application Number: US 09/924,358
; APPLICANT: Prior Filing Date: 2001-08-06
; APPLICANT: Prior Application Number: US 60/229,300
; APPLICANT: Prior Filing Date: 2000-09-01
; APPLICANT: Prior Application Number: US 10/350,553
; APPLICANT: Prior Filing Date: 2003-01-24
; APPLICANT: Prior Application Number: US 60/351,572
; APPLICANT: Prior Filing Date: 2002-01-24
; APPLICANT: Prior Application Number: US 09/966,614

; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US 60/238,054
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: US 10/281,094
 ; PRIOR FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: US 60/347,815
 ; PRIOR FILING DATE: 2001-10-29
 ; PRIOR APPLICATION NUMBER: US 10/076,535
 ; PRIOR FILING DATE: 2002-02-15
 ; REMAINING PRIOR Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 136
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 101
 ; LENGTH: 396
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
US-10-410-764-101
 Query Match 99.0%; Score 2083; DB 15; Length 396;
 Best Local Similarity 99.2%; Pred. No. 3e-167;
 Matches 393; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MGANTSRKPPVFDENEDVNFDHFBLRAIGKGSFGEBVCIQKNDTKKMCAMKYMNKQKCV 60
 Db 1 MGANTSRKPPVFDENEDVNFDHFBLRAIGKGSFGKVCIVQKNDTKKMYAMKYMNKQKCV 60
 Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSQDEEDMFMVVDLLGGDLRYHLQQN VHFKB 120
 Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSQDEEDMFMVVDLLGGDLRYHLQQN VHFKC 120
 Qy 61 ETVKLIFICELVMA LDYLNQRIIHRDMKPDNILLDEGHVHITDPNIAAMLPRETQITM 180
 Db 121 ETVKLIFICELVMA LDYLNQRIIHRDMKPDNILLDEGHVHITDPNIAAMLPRETQITM 180
 Qy 181 AGTKP YMAPEMFSSRKGAGYSFAVDWNSLGVTA YELLRGRGPYHRSSTS SKEIVHTFET 240
 Db 181 AGTKP YMAPEMFSSRKGAGYSFAVDWNSLGVTA YELLRGRGPYHRSSTS SKEIVHTFET 240
 Qy 241 TVVTYP SAWSQEMVSLKKLLEPNPDQRFSQLSDVQNFPMNDINWDAVFOKR LIPGFIP 300
 Db 241 TVVTYP SAWSQEMVSLKKLLEPNPDQRFSQLSDVQNFPMNDINWDAVFOKR LIPGFIP 300
 Qy 301 NKGRLNCDPTFELEMILESKPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHLD SVQKF1 360
 Db 301 NKGRLNCDPTFELEMILESKPLHKKKKRLAKKEKDMRKCDSSQTCLLQEHLD SVQKF1 360
 Qy 361 IFNREKVNRDFNKQOPNLALBQTKDQGEDGQ 392
 Db 361 IFNREKVNRDFNKQOPNLALBQTKDQVTTNGQ 392
 RESULT 10
 US-10-108-260A-2674
 ; Sequence 2674, Application US/10108260A
 ; Publication No. US20040005560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: NO. US20040005560A1 full length cDNA
 ; FILE REFERENCE: H1-A0106
 ; CURRENT APPLICATION NUMBER: US/10/108,260A
 ; CURRENT FILING DATE: 2002-03-27
 ; NUMBER OF SEQ ID NOS: 5458
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2674
 ; LENGTH: 358
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
US-10-108-260A-2674
 Query Match 86.2%; Score 1814; DB 15; Length 358;
 Best Local Similarity 99.4%; Pred. No. 1.3e-144;
 Matches 342; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MGANTSRKPPVFDENEDVNFDHFBLRAIGKGSFGEBVCIQKNDTKKMCAMKYMNKQKCV 60
 Db 1 MGANTSRKPPVFDENEDVNFDHFBLRAIGKGSFGKVCIVQKNDTKKMYAMKYMNKQKCV 60
 Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSQDEEDMFMVVDLLGGDLRYHLQQN VHFKB 120
 Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSQDEEDMFMVVDLLGGDLRYHLQQN VHFKC 120
 Qy 121 ETVKLIFICELVMA LDYLNQRIIHRDMKPDNILLDEGHVHITDPNIAAMLPRETQITM 180
 Db 121 ETVKLIFICELVMA LDYLNQRIIHRDMKPDNILLDEGHVHITDPNIAAMLPRETQITM 180

Qy 181 AGTKPMAPEMFSRKAGGYSFADVWNLGVTAYPELRLRRPYHRSSTSKEIVHTFET 240
 Db 181 AGTKPMAPEMFSRKAGGYSFADVWNLGVTAYPELRLRRPYHRSSTSKEIVHTFET 240

Qy 241 TTVTYPSSAQSQEMVSLKKLLEPQNPQLSDVQNFPMNDINWDAYFQRKLIPGPIP 300
 Db 241 TTVTYPSSAQSQEMVSLKKLLEPQNPQLSDVQNFPMNDINWDAYFQRKLIPGPIP 300

Qy 301 NKGRLLNCDPTFELEMILESKPLHKKKRCLAKKEKDMDRKCDSSQ 344
 Db 301 NKGRLLNCDPTFELEMILESKPLHKKKRCLAKKEKDMDRKCDSSQ 344

RESULT 11
 US-10-074-978A-158
 ; Sequence 158, Application US/10074978A
 ; Publication No. US20040010119A1

GENERAL INFORMATION:
 ; APPLICANT: Leite, Mario
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Guo, Xiaojia (Sasha)
 ; APPLICANT: Fernandes, Elma
 ; APPLICANT: Li, Li
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Liu, Xiahong
 ; APPLICANT: Casman, Stacie
 ; APPLICANT: Boldog, Ferenc
 ; APPLICANT: Paturajan, Meera
 ; APPLICANT: Blalock, Angela
 ; APPLICANT: Ballinger, Robert
 ; APPLICANT: Verner, Corine
 ; APPLICANT: Tchernev, Velizar T
 ; APPLICANT: Malyankar, Uriel M
 ; APPLICANT: Gusev, Vladimir
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Mezes, Peter S
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Heyes, Melvin P
 ; APPLICANT: Herrman, John
 ; APPLICANT: Pena, Carol E A
 ; APPLICANT: Shimbets, Richard A
 ; APPLICANT: Taupier Jr, Raymond J
 ; APPLICANT: Moore, No. US20040010119A1
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Stone, Dave
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Peyman, John
 ; APPLICANT: Smithson, Glenna
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-269
 ; CURRENT APPLICATION NUMBER: US/10/074,978A
 ; CURRENT FILING DATE: 2003-01-07
 ; PRIOR APPLICATION NUMBER: 60/268,221
 ; PRIOR FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: 60/335,109
 ; PRIOR FILING DATE: 2001-10-31
 ; PRIOR APPLICATION NUMBER: 60/276,703
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/330,293
 ; PRIOR FILING DATE: 2001-10-18
 ; PRIOR APPLICATION NUMBER: 60/322,127
 ; PRIOR FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: 60/280,899
 ; PRIOR FILING DATE: 2001-04-02
 ; PRIOR APPLICATION NUMBER: 60/310,797
 ; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/268,646
 ; PRIOR FILING DATE: 2001-02-14
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 547
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 158
 ; LENGTH: 414
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-074-978A-158

Query Match 68.3%; Score 1437.5; DB 15; Length 414;
 Best Local Similarity 69.7%; Pred. No. 8.6e-113;
 Matches 278; Conservative 38; Mismatches 64; Indels 19; Gaps 3;

Qy 1 MGANTSRKPPVFDENEDVNFDHFELRAIGKGSFGBCIVQKNDTCKMCAMKYMNKQKCV 60
 Db 1 MGGNHSHKPPVFDENEVNFDFQILRAIGKGSFGKVCIVQKRDTCKMYAMKYMNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEEHPPFLVNLWYSPQDEEDMFMVVDLLGGDLRHYLQQNVHFKE 120
 Db 61 ERDDEVNVFRRELQIMQGLEEHPPFLVNLWYSPQDEEDMFMVVDLLGGDLRHYLQQNVHFKE 120

Qy 121 BTVKLPICELVALDYLQONQRIIHRDMKPDNNILDEGHVHITDFNIAAMLPRETQITTM 180
 Db 121 GTVKLPICELALALBEYLQRYHHIHRDIKPDNNILDEGHVHITDFNIAVTVLKGSEKASM 180

Qy 181 AGTKPMAPEMFS-SRKGAGYSFAVDWNLGVTAYPELRLRRPYHRSSTSKEIVHTF 238
 Db 181 AGTKPMAPEVFOVTVDDGGPGYSVPDVWNLGVTAYPELRLRGWRPYBHSATPIDELNMF 240

Qy 239 ETIVVTPSAWSQEMVSLKKLLEPQNPQLSDVQNFPMNDINWDAYFQRKLIPGF 298
 Db 241 KVERVHYSSTWCAGMVSLLKKLLTQDPBSRSSLRDIQSMTYLADMNWDAYFPEKALMGP 300

Qy 299 IPNKGRLNCDPTPELEMILESKPLHKKKRCLAK-KEKDMRKCDSSQTCLJQEHLDSVQK 357
 Db 301 VBNKGRLNCDPTPELEMILESKPLHKKKRCLAKHRSRDSTKDSCLPGLHQCLBTVRK 360

Qy 358 EP11FNREKUNRDENKQROPNLALBQTKDOPQGEDQMNML 396
 Db 361 EP11FNREKLRQQ-----QGDGQLSDL 383

RESULT 12
 US-09-801-876B-4
 ; Sequence 4, Application US/09801876B
 ; Patent No. US20020127683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEARIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL001160
 ; CURRENT APPLICATION NUMBER: US/09/801,876B
 ; CURRENT FILING DATE: 2001-03-09
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 404
 ; TYPE: PRT
 ; ORGANISM: Mus Musculus
 ; US-09-801-876B-4

Query Match 67.8%; Score 1427; DB 9; Length 404;
 Best Local Similarity 69.5%; Pred. No. 6.4e-112;
 Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;

Qy 1 MGANTSRKPPVFDENEDVNFDHFELRAIGKGSFGBCIVQKNDTCKMCAMKYMNKQKCV 60
 Db 1 MGGNHSHKPPVFDENEVNFDFQILRAIGKGSFGKVCIVQKRDTCKMYAMKYMNKQKCV 60

Qy 61 -ERNEVRNVFKELQIMQGLEEHPPFLVNLWYSQDEEDDMFMVVDLLGGDLRHYLQQNVHFK 119

Db 61 QERDEVNRVPRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDFLLGGDLRYHLQQNVHFT 120
 Qy 120 EETVKLPICBLVMAVDLYQNQRIIHRDMKPDNNILLDEHGHVHTIDFNIAAMLPRETQITT 179
 Db 121 EGTVKLKYICELAALALEYLQRYHIIHRDIKPDPNILLDEHGHVHTIDFNIAVLKGSEKASS 180
 Qy 180 MAGTKPVMAPEMFS--SRKGAGYSFAVDWWSLGTVTAYELLGRRPYHISRSSTSKEIVHT 237
 Db 181 MAGTKPVMAPEMFS--SRKGAGYSFAVDWWSLGTVTAYELLGRRPYBTHSATPIDEILNM 240
 Qy 238 FETTVVTVPSSAWQEMVSLLKKLLEPNDQRFSQLSDVQNFPPYMNDINWDAVFQKRLLPG 297
 Db 241 FKVERVHYSSTWCEGMVSLLKKLTDQPESRSLSLRDIOSMTYLAADMNWDAVFKEALMPG 300
 Qy 298 FIPNKGRLNCDPTFELEMILESKPLHKKKKRRLAK-KEKDMRKCDSSQTCLLQEHLDSVQ 356
 Db 301 FVPNKGRLNCDPTFELEMILESKPLHKKKKRRLAKHRSRDSLTDSCPLANGHLLQQCLETVR 360
 Qy 357 KEPIIFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396
 Db 361 KEPIIFNREKLRQQ-----QGDGQLSDL 384

RESULT 13
 US-10-667-442-4
 ; Sequence 4, Application US/10667442
 ; Publication No. US20040043466A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; THEREOF
 ; FILE REFERENCE: CL001160DIV
 ; CURRENT APPLICATION NUMBER: US/10/254,869
 ; CURRENT FILING DATE: 2002-09-26
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 404
 ; TYPE: PRT
 ; ORGANISM: Mus Musculus
 ; US-10-254-869-4

Query Match 67.8%; Score 1427; DB 14; Length 404;
 Best Local Similarity 69.5%; Pred. No. 6.4e-112;
 Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;

Qy 1 MGANTSRKPPVFDENEDVNFDHFPEILRAIGKGSFGEVCIQKNDTKKMCAMKYMNNKQKCV 60
 Db 1 MGGNHSHKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKMYAMKYMNNKQKCV 60
 Qy 61 -ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDFLLGGDLRYHLQQNVHFK 119
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 Db 121 EGTVKLKYICELAALALEYLQRYHIIHRDIKPDPNILLDEHGHVHTIDFNIAVLKGSEKASS 180
 Qy 180 MAGTKPVMAPEMFS--SRKGAGYSFAVDWWSLGVTAXELLGRGPYHIRSSTSKEIVHT 237
 Db 181 MAGTKPVMAPEMFS--SRKGAGYSFAVDWWSLGVTAYBLLRGWRPYBIHSATPIDEILNM 240
 Qy 238 FETTVVTVPSSAWQEMVSLLKKLLEPNDQRFSQLSDVQNFPPYMNDINWDAVFQKRLLPG 297
 Db 241 FKVERVHYSSTWCEGMVSLLKKLTDQPESRSLSLRDIOSMTYLAADMNWDAVFKEALMPG 300
 Qy 298 FIPNKGRLNCDPTFELEMILESKPLHKKKKRRLAK-KEKDMRKCDSSQTCLLQEHLDSVQ 356
 Db 301 FVPNKGRLNCDPTFELEMILESKPLHKKKKRRLAKHRSRDSLTDSCPLANGHLLQQCLETVR 360
 Qy 357 KEPIIFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396
 Db 361 KEPIIFNREKLRQQ-----QGDGQLSDL 384

RESULT 14
 US-10-254-869-4
 ; Sequence 4, Application US/10254869
 ; Publication No. US20030027307A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; THEREOF
 ; FILE REFERENCE: CL001160DIV
 ; CURRENT APPLICATION NUMBER: US/10/254,869
 ; CURRENT FILING DATE: 2002-09-26
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4

Query Match 67.8%; Score 1427; DB 14; Length 404;
 Best Local Similarity 69.5%; Pred. No. 6.4e-112;
 Matches 278; Conservative 38; Mismatches 64; Indels 20; Gaps 4;

Qy 1 MGANTSRKPPVFDENEDVNFDHFPEILRAIGKGSFGEVCIQKNDTKKMCAMKYMNNKQKCV 60
 Db 1 MGGNHSHKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTKKMYAMKYMNNKQKCV 60
 Qy 61 -ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDFLLGGDLRYHLQQNVHFK 119
 Db 61 QERDEVRVNFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDFLLGGDLRYHLQQNVHFT 120
 Qy 120 EETVKLFICELVMAVDLYQNORIIHRDMKPDNNILLDEHGHVHTIDFNIAAMLPRETQITT 179
 Db 121 EGTVKLKYICELAALALEYLQRYHIIHRDIKPDPNILLDEHGHVHTIDFNIAVLKGSEKASS 180
 Qy 180 MAGTKPVMAPEMFS--SRKGAGYSFAVDWWSLGVTAXELLGRGPYHIRSSTSKEIVHT 237
 Db 181 MAGTKPVMAPEMFS--SRKGAGYSFAVDWWSLGVTAYBLLRGWRPYBIHSATPIDEILNM 240
 Qy 238 FETTVVTVPSSAWQEMVSLLKKLLEPNDQRFSQLSDVQNFPPYMNDINWDAVFQKRLLPG 297
 Db 241 FKVERVHYSSTWCEGMVSLLKKLTDQPESRSLSLRDIOSMTYLAADMNWDAVFKEALMPG 300
 Qy 298 FIPNKGRLNCDPTFELEMILESKPLHKKKKRRLAK-KEKDMRKCDSSQTCLLQEHLDSVQ 356
 Db 301 FVPNKGRLNCDPTFELEMILESKPLHKKKKRRLAKHRSRDSLTDSCPLANGHLLQQCLETVR 360
 Qy 357 KEPIIFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396
 Db 361 KEPIIFNREKLRQQ-----QGDGQLSDL 384

RESULT 15
 US-09-801-878-5
 ; Sequence 5, Application US/09801878
 ; Patent No. US20020127683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; THEREOF
 ; FILE REFERENCE: CL001160
 ; CURRENT APPLICATION NUMBER: US/09/801,878
 ; CURRENT FILING DATE: 2001-03-09
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 403

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; TYPE: PRT
; ORGANISM: Human
US-09-801-876B-5

Query Match 67.8%; Score 1425.5; DB 9; Length 403;
Best Local Similarity 68.2%; Pred. No. 8.5e-112;
Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

Qy   1 MGANTSRKPPVPPDENEDVNFDHFELRAIGKGSFGEYCTIVQONDTKKMCAMCYMNQKCV 60
Db    1 MGGNHSRKPPVPPDENEEVNFDHFQILRAIGKGSFHKVCIHQKRTDKKMCAMCYMNQKCVI 60

Qy   61 ERNEVRNVPKEBLQIMQGLEHPPFLVNLWYSFQDEEDDMFMVVDLILLGGDLRHYLQONWHPKS 120
Db    61 ERDEVNVRNFRELQIMQGLEHPPFLVNLWYSFQDDEDMFMVVDLILLGGDLRHYLQONWHPTE 120

Qy   121 ETVICLFIGCLVMAVDYLQNQRIIHRDMKPDNILLDEHGHVHTIDFNIAAMLPRETOITM 180
Db    121 GTVKLYICBLAIALEYLQRYHTIHRDIKPDNILLDEHGHVHTIDFNIAATVKGAEERASSM 180

Qy   181 AGTKPAMYAPEMPS--SRKGAGYSPAVDWWSLGVAYBLLGRRPYHIRSTSSKEIVHTP 238
Db    181 AGTKPAMYAPEVQVMDRGPGSYSPVDDWWSLGITAYELLGRPYEIHSSVTPIDEILNMF 240

Qy   239 ETTVVVTYPSAWSQEMVSLLKKLEPNPDQRFSQLSDVQNFPYMMNDINWDAVFOKRLIPGF 298
Db    241 KVERVHYSSTWCCKGMVALRKLTQDPESRVSSLHDIQSVPLADMNWDAVFKKALMPGF 300

Qy   299 IPNKGRLNCDPTEBLEEMILESKPLHKKERLAK-KEKOMRKCDSSQTCLLQEHLDVQK 357
Db    301 VPNKGRLNCDPTEBLEEMILESKPLHKKERLAKNSRDGTKDSCPLNGHLQHCLETVRE 360

Qy   358 EPIIFNREKVNRDFNKRQPNLALEQTKDPOG---EDGQNNNL 396
Db    361 EPIIFNREKLRRQQGQGSQQLTDSSRGGQAQSKLQDGCGNNNL 403

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Search completed: June 25, 2004, 10:56:33
Job time : 49 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 25, 2004, 10:48:00 ; Search time 23 seconds

(without alignments)
 888.865 Million cell updates/sec

Title: US-10-667-442-2

Perfect score: 2104

Sequence: 1 MGANTSRKPPVFDENEDVNF.....NLALEOTKDQGEDGQNNL 396

Scoring table: BLOSUM62

Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:
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 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:
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 6: /cgn2_6/ptodata/2/iaa/backfile1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2104	100.0	396	4	US-09-801-876B-2	Sequence 2, Appli
2	2104	100.0	396	4	US-10-254-869-2	Sequence 2, Appli
3	2089	99.3	396	4	US-09-841-683-11	Sequence 11, Appli
4	2047	97.3	407	4	US-09-841-683-9	Sequence 9, Appli
5	1427	67.8	404	4	US-09-801-876B-4	Sequence 4, Appli
6	1427	67.8	404	4	US-10-254-869-4	Sequence 4, Appli
7	1425.5	67.8	403	4	US-09-801-876B-5	Sequence 5, Appli
8	1425.5	67.8	403	4	US-10-254-869-5	Sequence 5, Appli
9	1324	62.9	419	4	US-09-799-875-14	Sequence 14, Appli
10	1317.5	62.6	384	4	US-09-801-876B-6	Sequence 6, Appli
11	1317.5	62.6	384	4	US-10-254-869-6	Sequence 6, Appli
12	1278.5	60.8	399	4	US-09-819-607-4	Sequence 4, Appli
13	1161	55.2	236	4	US-09-841-683-7	Sequence 7, Appli
14	1158	55.0	225	4	US-09-841-683-5	Sequence 5, Appli
15	1137.5	54.1	369	4	US-09-819-607-2	Sequence 2, Appli
16	1122.5	53.4	368	4	US-09-819-607-5	Sequence 5, Appli
17	1010.5	48.0	316	4	US-09-801-876B-7	Sequence 7, Appli
18	1010.5	48.0	316	4	US-10-254-869-7	Sequence 8, Appli
19	843.5	40.1	347	4	US-09-801-876B-8	Sequence 8, Appli
20	843.5	40.1	347	4	US-10-254-869-8	Sequence 2, Appli
21	498.5	23.7	336	4	US-09-394-455-2	Sequence 15, Appli
22	498.5	23.7	343	4	US-09-394-455-15	Sequence 34, Appli
23	498.5	23.7	343	4	US-09-394-455-34	Sequence 4, Appli
24	498.5	23.7	351	4	US-09-394-455-4	Sequence 2, Appli
25	495.5	23.6	587	1	US-08-313-274-2	Sequence 18, Appli
26	493.5	23.5	689	1	US-08-221-817-18	Sequence 18, Appli
27	493.5	23.5	689	1	US-08-454-439-18	Sequence 18, Appli

RESULT 1 US-09-801-876B-2							
; Sequence 2, Application US/09801876B							
; Patent No. 6492155							
; GENERAL INFORMATION:							
; APPLICANT: YE, Jane et al							
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES							
; TITLE OF INVENTION: THEREOF							
; FILE REFERENCE: CL001160							
; CURRENT APPLICATION NUMBER: US/09/801,876B							
; CURRENT FILING DATE: 2001-03-09							
; NUMBER OF SEQ ID NOS: 8							
; SOFTWARE: FastSEQ for Windows Version 4.0							
; SEQ ID NO 2							
; LENGTH: 396							
; TYPE: PRT							
; ORGANISM: Human							
US-09-801-876B-2							
Query Match Score 100.0%; Score 2104; DB 4; Length 396;							
Best Local Similarity 100.0%; Pred. No. 1.6e-194; Mismatches 0; Indels 0; Gaps 0;							
Matches 396; Conservative 0; MisMatches 0;							
Qy	1	MGANTSRKPPVFDENEDVNFDFEFLRAIGKGSFGEVCIVQKNDTKKMCAMCYMNKRQKCV	60	Db	1	MGANTSRKPPVFDENEDVNFDFEFLRAIGKGSFGEVCIVQKNDTKKMCAMCYMNKRQKCV	60
Qy	1	MGANTSRKPPVFDENBDVNFDHFBLRAIGKGSFGEVCIVQKNDTKKMCAMCYMNKRQKCV	60	Db	1	ERNEVRNVFKELQIMQGLEHFPFLVNLWYSFQDEEDMFMVYDILGGDLRYHLQQNVHFKC	120
Qy	61	ERNEVRNVFKELQIMQGLEHFPFLVNLWYSFQDEEDMFMVYDILGGDLRYHLQQNVHFKC	120	Db	61	ERNEVRNVFKELQIMQGLEHFPFLVNLWYSFQDEEDMFMVYDILGGDLRYHLQQNVHFKC	120
Qy	61	ETVKLFICELVMALDYLQNORI IHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM	180	Db	121	AGTKPYPMAPEMFSSRKGAGYSFAVDWMSLGVTAYPELLRGRPRPYHRSSTSKEIVHTFET	240
Qy	121	ETVKLFICELVMALDYLQNORI IHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM	180	Db	121	AGTKPYPMAPEMFSSRKGAGYSFAVDWMSLGVTAYPELLRGRPRPYHRSSTSKEIVHTFET	240
Qy	181	AGTKPYPMAPEMFSSRKGAGYSFAVDWMSLGVTAYPELLRGRPRPYHRSSTSKEIVHTFET	240	Db	181	AGTKPYPMAPEMFSSRKGAGYSFAVDWMSLGVTAYPELLRGRPRPYHRSSTSKEIVHTFET	240
Qy	181	AGTKPYPMAPEMFSSRKGAGYSFAVDWMSLGVTAYPELLRGRPRPYHRSSTSKEIVHTFET	240	Db	181	AGTKPYPMAPEMFSSRKGAGYSFAVDWMSLGVTAYPELLRGRPRPYHRSSTSKEIVHTFET	240
Qy	241	FVVTYPSAWSQEMVSLLKLLBNPDRQFSQLSDVQNFPMNDINWDAYPKRLIPGFIP	300	Db	241	FVVTYPSAWSQEMVSLLKLLBNPDRQFSQLSDVQNFPMNDINWDAYPKRLIPGFIP	300
Qy	241	FVVTYPSAWSQEMVSLLKLLBNPDRQFSQLSDVQNFPMNDINWDAYPKRLIPGFIP	300	Db	241	NKGRLNCDPTFELEEMILESKPLHKKKKRLLAKKEKDMRKCDSSQTCLLQEHLDSSVQKEFI	360
Qy	301	NKGRLNCDPTFELEEMILESKPLHKKKKRLLAKKEKDMRKCDSSQTCLLQEHLDSSVQKEFI	360	Db	301	NKGRLNCDPTFELEEMILESKPLHKKKKRLLAKKEKDMRKCDSSQTCLLQEHLDSSVQKEFI	360
Qy	361	IFNRBKVNRDFNKRQPNLALBQTKDPOGBDQNNNL 396	1	Qy	361	IFNRBKVNRDFNKRQPNLALBQTKDPOGBDQNNNL 396	1

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

RESULT 2
US-10-254-869-2
; Sequence 2, Application US/10254869

; GENERAL INFORMATION:

; APPLICANT: YE, Jane et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USSES

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USSES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001160DIV

; CURRENT APPLICATION NUMBER: US/10/254,869

; CURRENT FILING DATE: 2002-09-26

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 396

; TYPE: PRT

; ORGANISM: Human

US-10-254-869-2

Query Match 100.0%; Score 2104; DB 4; Length 396;

Best Local Similarity 100.0%; Pred. No. 1..6e-194; Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIYQKNDTCKMCAKYMNNKQKCV 60

Db 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIYQKNDTCKMCAKYMNNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHFFLYNLWYSFQDEEDMFMDVLLGGDLRYHLQQNTHFKE 120

Db 61 ERNEVRNVFKELQIMQGLEHFFLYNLWYSFQDEEDMFMDVLLGGDLRYHLQQNTHFKE 120

Qy 121 ETVKLKFLICELVMAVDYLQNQRIIHRDMKPDNILLDEHGHVHITDENIAAMLPRETOJTTM 180

Db 121 ETVKLKFLICELVMAVDYLQNQRIIHRDMKPDNILLDEHGHVHITDENIAAMLPRETOJTTM 180

Qy 181 AGTKPYYMAPEMPSRSRKGAGYSFAYDWNSLGVTAYELLGRGPYHRSSTSSEKIVHTFET 240

Db 181 AGTKPYYMAPEMPSRSRKGAGYSFAYDWNSLGVTAYELLGRGPYHRSSTSSEKIVHTFET 240

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 396
; TYPE: PRT
; ORGANISM: homo sapiens
; us-09-841-683-11

Query Match 99.3%; Score 2089; DB 4; Length 396;

Best Local Similarity 99.5%; Pred. No. 4..4e-193; Matches 394; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIYQKNDTCKMCAKYMNNKQKCV 60

Db 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIYQKNDTCKMCAKYMNNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHFFLYNLWYSFQDEEDMFMDVLLGGDLRYHLQQNTHFKE 120

Db 61 ERNEVRNVFKELQIMQGLEHFFLYNLWYSFQDEEDMFMDVLLGGDLRYHLQQNTHFKE 120

Qy 121 ETVKLKFLICELVMAVDYLQNQRIIHRDMKPDNILLDEHGHVHITDENIAAMLPRETOJTTM 180

Db 121 ETVKLKFLICELVMAVDYLQNQRIIHRDMKPDNILLDEHGHVHITDENIAAMLPRETOJTTM 180

Qy 181 AGTKPYYMAPEMPSRSRKGAGYSFAYDWNSLGVTAYELLGRGPYHRSSTSSEKIVHTFET 240

Db 181 AGTKPYYMAPEMPSRSRKGAGYSFAYDWNSLGVTAYELLGRGPYHRSSTSSEKIVHTFET 240

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Db 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Db 241 TTVTYPSSAWSQEMVSLKKLLEPNPDPQRFSQLSDVQNFPMNDINWDVQKRLIPPGFIP 300

Qy 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Db 301 NKGRILNCDPTPELEMILESKPLHKKKKRKLAKKEKDMDRKCDSSQTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKROPNLALLEQTKDQQGEDGQNNNL 396

Qy 1 MGANTSRKPPVFDENEDVNFDHFPEILRAIGKGSFGEVCIVQNDTKKMCAMCKMNRKCV 60
Db 1 MGANTSRKPPVFDENEDVNFDHFPEILRAIGKGSFGEVCIVQNDTKKMCAMCKMNRKCV 60

Qy 61 ERNEYTRNVFKELQIMQGLEHPFLVLWYSFQDEEDDMFMVTDLILGGDLRYHLQONVHFK 120
Db 61 ERNEYTRNVFKELQIMQGLEHPFLVLWYSFQDEEDDMFMVTDLILGGDLRYHLQONVHFK 120

Qy 121 ETVKLPCICBLVMAVDLYLQNORIIHRDMKPDNILLDEHGHVHITDFNIAAMLPREQTITM 180
Db 121 ETVKLPCICBLVMAVDLYLQNORIIHRDMKPDNILLDEHGHVHITDFNIAAMLPREQTITM 180

Qy 181 AGTKPIMAPEMFSSRKKGAGYSFAVDWWSLGVTAYELLRGRRPYHRSSTSKEIVHTFET 240
Db 181 AGTKPIMAPEMFSSRKKGAGYSFAVDWWSLGVTAYELLRGRRPYHRSSTSKEIVHTFET 240

Qy 241 TVVTPSAWSQEMVSLKICLLEPQLNPSQDQRFSQLSDVQNFPMNDINWDAVFQKRLLIPGFIP 300
Db 241 TVVTPSAWSQEMVSLKICLLEPQLNPSQDQRFSQLSDVQNFPMNDINWDAVFQKRLLIPGFIP 300

Qy 301 NKGRLNCDPTFELBEMILESKPLHKKKCRCLAKKEKDMDRKCDSSOTCLLQEHLDSVQKEFI 360
Db 301 NKGRLNCDPTFELBEMILESKPLHKKKCRCLAKKEKDMDRKCDSSOTCLLQEHLDSVQKEFI 360

Qy 361 IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQ 392
Db 361 IFNREKVNRDFNKRQPNLALEQTKDPOGEDGQ 392

US-10-254-869-4

RESULT 6

Qy 1 MGANTSRKPPVFDENEDVNFDHFPEILRAIGKGSFGEVCIVQNDTKKMCAMCKMNRKCV 60
Db 1 MGGNHSHKPPVFDENEDVNFDHFPEILRAIGKGSFGEVCIVQNDTKKMCAMCKMNRKCV 60

Qy 61 -ERNEYTRNVFKELQIMQGLEHPFLVLWYSFQDEEDDMFMVTDLILGGDLRYHLQONVHFK 119
Db 61 QERDEVNVFRELQIMQGLEHPFLVLWYSFQDEEDDMFMVTDLILGGDLRYHLQONVHFT 120

Qy 120 BETVKLPCICBLVMAVDLYLQNORIIHRDMKPDNILLDEHGHVHITDFNIAAMLPREQTIT 179
Db 121 EGTVKLPCICBLVMAVDLYLQNORIIHRDMKPDNILLDEHGHVHITDFNIAAMLPREQTIT 180

Qy 180 MAGTKPIMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLRGRRPYHRSSTSKEIVHT 237
Db 181 MAGTKPIMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLRGRRPYHRSSTSKEIVHT 237

Qy 238 FETTVVTYPSAWSQEMVSLKICLLEPQLNPSQDQRFSQLSDVQNFPMNDINWDAVFQKRLLPG 297
Db 241 FKVERVHYSSSTWCEGMVSLLKQLLTQDPESRLSSLRDIQSMTYLADMNWDAVFQKRLLPG 300

Qy 298 FIPNKGRLNCDPTFELBEMILESKPLHKKKCRCLAKKEKDMDRKCDSSOTCLLQEHLDSVQ 356
Db 301 FIPNKGRLNCDPTFELBEMILESKPLHKKKCRCLAKKEKDMDRKCDSSOTCLLQEHLDSVQ 356

Qy 357 KEPFIFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396
Db 361 KEPFIFNREKVNRDFNKRQPNLALEQTKDPOGEDGQNNNL 396

US-10-254-869-4

RESULT 7

Qy 1 MGANTSRKPPVFDENEDVNFDHFPEILRAIGKGSFGEVCIVQNDTKKMCAMCKMNRKCV 60
Db 1 MGGNHSHKPPVFDENEDVNFDHFPEILRAIGKGSFGEVCIVQNDTKKMCAMCKMNRKCV 60

Qy 61 QERDEVNVFRELQIMQGLEHPFLVLWYSFQDEEDDMFMVTDLILGGDLRYHLQONVHFT 120

Qy 120 BETVKLPCICBLVMAVDLYLQNORIIHRDMKPDNILLDEHGHVHITDFNIAAMLPREQTIT 179
Db 121 EGTVKLPCICBLVMAVDLYLQNORIIHRDMKPDNILLDEHGHVHITDFNIAAMLPREQTIT 179

Qy 180 MAGTKPIMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLRGRRPYHRSSTSKEIVHT 237
Db 181 MAGTKPIMAPEMFS--SRKGAGYSFAVDWWSLGVTAYELLRGRRPYHRSSTSKEIVHT 237

Qy 238 FETTVVTYPSAWSQEMVSLKQLLTQDPESRLSSLRDIQSMTYLADMNWDAVFQKRLLPG 297
Db 241 FKVERVHYSSSTWCEGMVSLLKQLLTQDPESRLSSLRDIQSMTYLADMNWDAVFQKRLLPG 300

CURRENT APPLICATION NUMBER: US/09/801,876B
 CURRENT FILING DATE: 2001-03-09
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5
 LENGTH: 403
 TYPE: PRT
 ORGANISM: Human
 US-09-801-876B-5

Query Match 67.8%; Score 1425.5; DB 4; Length 403;
 Best Local Similarity 68.2%; Pred. No. 4.1e-129;
 Matches 275; Conservative 44; Mismatches 77; Indels 7; Gaps 3;

Qy 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCKAMKYMNMKQKCV 60
 Db 1 MGGNHSHHKPPVFDENEEVNFDHFQILRAIGKGSFGKVCIVQKRDTRKAMKYMNMKQKCI 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDEDMFMVVDLGGDLRYHLQONTWFKB 120
 Db 61 ERDEVRNVFRELQIMQGLEHPFLVNLWYSFQDEDEDMFMVVDLGGDLRYHLQONTWFTB 120

Qy 121 BTVKLPICELVMALDYLQONRIIHRDMKPDNILLDEHGHVHTIDENIAAMLPRETQITM 180
 Db 121 GTVLYCICELLALEYLQRYHIIHRDTKPDNILLDEHGHVHTIDENIAVTKGAERASSM 180

Qy 181 AGTKPYPMAPEMFS--SRKGAGYSFAVDWSSLGVTAYELLOWKRRPYHRSSTSKEIVHTF 238
 Db 181 AGTKPYPMAPEVFQVYMDRGPQGYSVPDVNLWYSFQDEEDMFVVDLGGDLRYHLQONTWFK 240

Qy 239 ETTVVVTYPSAWSQEMVSLLKKLLEPDPQRFSQLSDVQNFPYMDINWDAVFKRLLIPGP 298
 Db 241 KVERVHYSSSTWCKGMVALLRKLLTQDPESRVSSLHDIQSVPLADMNWDAVFKKALMPGP 300

Qy 299 IPNKGRNLNCDPTELEMILESKPLHKKKKRLLAK-KEKDMDRKCDSSQTCLQEHLDSVQK 357
 Db 301 VPNKGRNLNCDPTELEMILESKPLHKKKKRLLAKNRNSRDGTKDSCPVLNGHLQHCLTVE 360

Qy 358 EFIIFNREKVNRDFNKRQPNLALEQTKDPOG---EDGQNNNL 396
 Db 361 EFIIFNREKLRQQGGSQLLTDTSRGQQAQSQKLDQDGCMNNL 403

RESULT 9
 US-09-799-875-14
 Sequence 14, Application US/09799875
 ; Patent No. 6638721
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyers, Rachel
 ; APPLICANT: Kapeller-Liebermann, Rosana
 ; APPLICANT: Williamson, Mark
 ; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
 ; TITLE OF INVENTION: Therefor
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/799,875
 ; CURRENT FILING DATE: 2001-03-06
 ; PRIOR APPLICATION NUMBER: 60/182,059
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 09/659,287
 ; PRIOR FILING DATE: 2000-09-12
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 14
 ; LENGTH: 419
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-799-875-14

Query Match 62.9%; Score 1324; DB 4; Length 419;
 Best Local Similarity 64.5%; Pred. No. 2.7e-119;
 Matches 53; Mismatches 77; Indels 10; Gaps 4;

Qy 1 MGANTSRKPPVFDENEDVNFDHFEILRAIGKGSFGEVCIVQKNDTKKMCKAMKYMNMKQKCV 60
 Db 5 MSAATARR-PVFDKEDVNFDHFQILRAIGKGSFGEVCIVQKNDTKKMCKAMKYMNMKQKCI 63

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLGGDLRYHLQONTWFK 120
 Db 64 ERDEVNVFRELQIEHFLQVPLVNLWYSFQDEEDMFVVDLGGDLRYHLQONTWFK 123

Qy 121 BTVKLPICELVMALDYLQONRIIHRDMKPDNILLDEHGHVHTIDENIAAMLPRETQITM 180
 Db 124 DTVRLYCEMALADYLQGHHITRDVKPDNILLDERGHAHLTIDENIATIKDGERATAL 183

Qy 181 AGTKPYPMAPEMFS--RKKGAGYSFAVDWSSLGVTAYELLOWKRRPYHRSSTSKEIVHTF 238
 Qy 239 ETTVVVTYPSAWSQEMVSLLKKLLEPDPQRFSQLSDVQNFPYMDINWDAVFKRLLIPGP 298
 Db 244 STVSQVTPWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVWLDSVQ 303

Qy 299 IPNKGRNLNCDPTELEMILESKPLHKKKKRLLAK-KEKDMDRKCDSSQTCLQEHLDSVQ 356

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
; US-10-254-869-6

RESULT 13
US-09-841-683-7
; Sequence 7, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 236
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-841-683-7

RESULT 14
US-09-841-683-5 Sequence 5, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walko, D. Wade
; TITLE OF INVENTION: No. 6617147ei Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-5

Query Match Score 1158; DB 4; Length 225;
Best Local Similarity Pred. No. 1.1e-103;
Matches 218; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1 MGANTSRKPPVFDENEDVNPDHFEILRAIGKGSFGEVCIQKNPDTKQMCAMKYMNKOKCV	60
Db	1 MGANTSRKPPVFDENEDVNPDHFEILRAIGKGSFGKVCIQKNPDTKQMYAMCQYMKOKCV	60
Qy	61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDDMFMVVDLLGGDLRHYHLQQNVHFKE	120
Db	61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDDMFMVVDLLGGDLRHYHLQQNVHFKE	120
Qy	121 ETVKLFIGELVMAODYLQNQRIIHRDMKPDNILLDEHGIVHITDFNIAAMLPRETQITTM	180
Db	121 ETVKLFIGELVMAODYLQNQRIIHRDMKPDNILLDEHGIVHITDFNIAAMLPRETQITTM	180
Qy	181 AGTKPYPMAPEMFSSRKGAGYSFAVDWWSLGVTVAYELLRGR	220
Db	181 AGTKPYPMAPEMFSSRKGAGYSFAVDWWSLGVTVAYELLRGR	220

RESULT 15
US-09-819-607-2
; Sequence 2, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEARIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION:
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Human
; US-09-819-607-2

Query Match 54.1%; Score 1137.5; DB 4; Length 369;
Best Local Similarity 62.8%; Pred. No. 2.1e-101;
Matches 218; Conservative 47; Mismatches 73; Indels 9; Gaps 3;
QY MCAMKTMNKQKCVERNEVRNVIKELQIMQGLEHPPFLVNLWYSFQDDEEDMFMVVDLLGGD 107

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Db      1 MYAMKYMNKQQC1IERDEVRNVFREBLEBILQIEHVFVNWLWYSFQDEEDMFMVVDLLGGD 60
Qy      108 LRYTHLQQNVHFKEETVKLFICELYMALDYLNQRITIHRDMKPDNILLDEIGHVHITDFNI 167
Db      61 LRYHQQNVQFSEDTVRLYICEMALALDYLRGQHIIHRDVCPDNILLDERGHAAHLTDFNI 120
Qy      168 AAMLPRETQITTMAGTKPYYMAPEMPSS - RKGAGYSFAVDWWSLGVTAELLRGRRPYHI 225
Db      121 ATIIDGERATAAGTKPYYMAPEIPHSFVNGGTGXSFEVDDWWSVGVMAYELLRGWRPYDI 180
Qy      226 RSSTSKEIVHTPPTVVVTPSAWSQEMVSLLKKLEPNPDQRFSQLSDVQNFPYMDIN 285
Db      181 HSSNAVESLVOLFSTSVQVPTWSKEMVALRKLLTVNPERHRLSSLQDVOAAPALAGVL 240
Qy      286 WDAVFQKRLIPGPPIPNKGRLNCDPTELEEMILESPLHKKKRLAKKEKDMRKCDSSQT 345
Db      241 WDHLSSEKRVEPGVPNKGRLHCDPTFELEEMILESPLHKKKRLAKNKSRDNSRDSQS 300
Qy      346 --CLLQEHDSDVQKEFIIFNREKVNRDFNKRQPNLALEOTKDPQGED 390
Db      301 ENDYLQDCLDIAIQQDFVIFNREKL-----KRSQDLPREPLPAPERSRD 342

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Search completed: June 25, 2004, 10:51:42
 Job time : 25 secs